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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                   Copyright
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- protein search, using sw model OM protein

; Search time 218.8/2 occurred (without alignments)
1282.772 Million cell updates/sec Search time 218.872 Seconds February 28, 2006, 08:37:25 Run on:

US-10-717-665A-44 3349° · 1 MPQPSVSGMDPPFGDAFRSH.....TAEGNPTGGLVGLRIPTSKV 639 Title: Perfect score:

Sequence:

2443163 segs, 439378781 residues Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table: Searched: 2443163

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* geneseqp2004s:* geneseqp2004s:* geneseqp1980s:* A Geneseq 21:* 4.0.00 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description			Novel	Ado20373 Human PRO	Adk35935 Novel hum	Abp64928 Human pro	Abb68374 Drosophil	Adk65836 Angiogene	Ade61623 Rat Prote	Add46090 Rat Prote			Abg29275 Novel hum		0	Aab62331 Amino aci		Adj65096 HHV8 late	Adv68154 Kaposi's	Aae37016 Human nuc	Aaw01897 Nonsense-	Aay98056 Yeast NMD	Aaw01896 Nonsense-	Aay05835 Yeast Nmd	Aay98055 Yeast Nmd
: E		ADK65805	ADQ66472	AD020373	ADK35935	ABP64928	ABB68374	ADK65836	ADE61623	ADD46090	ADE57828	ADE57830	ABG29275	AAY96255	AAY58500	AAB62331	ABB05621	ADJ65096	ADV68154	AAE37016	AAW01897	AAY98056	AAW01896	AAY05835	AAY98055
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AAB85725	ABP73549	\EB22174	AAM39101	AAM40887	ADD01163	ABP96961	JDP46649	\DP46648	IDE61625	\DD46092	JAR79912	LAW84052	JAB48964	\DD49220	ADJ58974	4DP54086	4DY19864	ABM80398	ABG09944	4BM87025	
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842	427	3553	1279	1305	709	2724	520	568	706	106	707	707	707	707	707	707	707	710	2097	722	
5.4	5.3	5.3	5.3	<u>س</u>	2.5	5.2	5.2	5.2	5.2	5.2	5.2	2.5	5.2	2	5.2	2.5	2.5	2.5	5.2	5.2	
181	179	179	178.5	178.5	175.5	175	174	174	174	174	174	174	174	174	174	174	174	174	173.5	172.5	
25	26	27	28	6	30	31	32	33	34	32	36	37	8	36	4	41	4	43	4	45	

ALIGNMENTS

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Angiogenesis-differentially expressed protein ANH0757.
  ADK65805 standard; protein; 639 AA
            06-MAY-2004 (first entry)
       ADK65805;
ADK65805
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cytostatic; cardiant; vasotropic; antiarteriosclerotic; angiogenesis inhibitor; angiogenesis stimulator; angiogenesis stimulator; angiogenic index; gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine.

Homo sapiens.

WO2003066831-A2.

14-AUG-2003.

07-FEB-2002; 2002US-00067482. 10-JUN-2002; 2002US-00164595. 16-AUG-2002; 2002US-0403649P. 03-JAN-2003; 2003US-0437746P. 07-FEB-2003; 2003WO-US003848

(ORIG-) ORIGENE TECHNOLOGIES INC.

Jay Fan W, Li X, Kovacs KF, Sun Z,

ö

WPI; 2003-731502/69. N-PSDB; ADK65804. Determining the anglogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial ischemia and/or arteriosclerosis.

Claim 23; SEQ ID NO 44; 296pp; English.

The invention relates to a method of determining the anglogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the anglogenic index. The methods and compositions of the present

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EP1440981-A2

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invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary arteriosaclerosis. They can also be used in research, drug discovery and forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
                                                                                                                                                                                        SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEED
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                                                                                                                100.0%; Score 3349; DB 7;
100.0%; Pred. No. 8.4e-248;
iive 0; Mismatches 0;
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Matches 639; Conservative
                                                                                       Sequence 639 AA;
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osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
            Æ
                                                                                      Novel human protein sequence #1445
            417
         ADQ66472 standard; protein;
                                                            07-OCT-2004
ADQ66472
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AD020373

sapiens

cancer Ношо

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The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% or 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein sequence of the invention.
                                                                                                                                                                                                                                                                     Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases. Alzheimer's diseases, Parkinson's diseases, dementia and various cancers
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Pred. No. 6.5e-156;
0; Mismatches 1;
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                                                                         21-JAN-2004; 2004EP-00001196
                                                                                                    21-JAN-2003; 2003JP-00102206
09-MAY-2003; 2003JP-00131392
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                                                                                                                                                                               Sugiyama T,
                                                                                                                                                                                           Isono Y,
                                                                                                                                                                                                                         2004-535376/52.
                                                                                                                                                                                                                                         N-PSDB; ADQ64284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 417 AA;
                                                                                                                                                                                               Yamamoto J,
                                           28-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                    Novel PRO polypeptide e.g., PRO69614, PRO711106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                              rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, duillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQGRMLRPSEWNRDTLPSN
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                                                       PRO; immune related disorder; systemic lupus erythematosus;
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Pred. No. 5.1e-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; SEQ ID NO 1266; 1731pp; English.
                                                                                                                                                                                                                                                                                                   Chiu H,
                                                                                                                                                                                                                                                                                                    Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.8%;
                                                                                                                                                                                                                                 06-NOV-2003; 2003WO-US035268
                                                                                                                                                                                                                                                     08-NOV-2002; 2002US-0425235P
                                Human PRO polypeptide #633
         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 294; Conservative
                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                         spondyloarthropathy.
                                                                                                                                                                                                                                                                                                                                      WPI; 2004-420067/39.
N-PSDB; ADO20372.
                                                                                                                                                                                                                                                                                                    Dennis K,
Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 296 AA;
                                                                                                                                                                                   WO2004043361-A2
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                   Fong S, I
Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
셤
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This invention relates to a novel isolated polynucleotide comprising a nucleotide sequence selected from one of 1680 sequences, a mature protein coding portion of them, an active domain of them and their complementary sequences. The invention may be useful for the production of compounds with an antiarthritic, antiparkinsonian, neuroprotective, nootropic, immunosuppressive, cytostatic, antipsoriatic, antipfarmatory, antibacterial, antiviral, antifungal or antiparasitic activity. In addition, the disclosed sequences may be useful for gene therapy. The polypeptides or their antibodies are useful for treating many diseases such as arthitis, Parkinson's, Alzheimer's autinimume diseases, cancer, psoriasis, inflammatory bowel disease and infections caused by bacteria, viruses, fundi or parasites. The present sequence is that of a human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's disease, and inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .256
/label= OTHER
/note= "OTHER= All Xaa's in this sequence are unknown
amino acids or the site of a stop codon within the DNA
584 ERGPNMGQKLBILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 639
241 ERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunosuppressive; cytostatic; antipsoriatic; antiinflammatory; antibacterial; antiviral; antifungal; antiparasitic; gene therapy; arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer; psoriasis; inflammatory bowel disease; infection; bacteria; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiarthritic; antiparkinsonian; neuroprotective; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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98.8%; Pred. No. 1.1e-88;
iive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claim 20; SEQ ID NO 8017; 504pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human polypeptide SegID8017.
                                                                                                                                                                                                                                             ADK35935 standard; protein; 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-2001; 2001WO-US004941.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-MAR-2000; 2000US-00519705.
19-MAY-2000; 2000US-00574454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                    06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 98.8
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungus; parasite; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-280918/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200216439-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                 ADK35935;
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                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                 ADK35935
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Disclosure; SEQ ID NO 31914; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.8
Best Local Similarity 100.
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                          Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABL12477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB68374;
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ID ABB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel human coding sequences (ABQ99268-ABQ99608) and proteins (ABP64662-ABP65022). The sequences are useful in therapeutic, diagnostic and research methods. The polynucleotides may be used in the field of molecular biology as hybridisation probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The polynucleotides are useful in diagnostics as expressed sequence tags (EST9) for identifying expressed genes or for physical mapping of the human genome. The proteins may be used as molecular weight markers, or as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; expressed sequence tag; BST; haematopoietic disorder; central nervous system disease; viral infection, peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; nootropic; antiallergyc, antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide; immunostimmlant; cerebroprotective.
                                                                          282
                                                                                                                                                  342
                                                                                             EKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPL 124
                                                                                                                                                                        125 QGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVS 184
                                                                                                                                                                                                                          402
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                                   64
                           5 VKQNPLPSSFPGKKITIRLAAPVCSSKTLQAEVPLSDCVQKASKPTSSTQIMVKINMYHN
                                                                                                                                                                                                                                              DNLGEQPTKCSPEEDEEDTEDVDDEDHDEGFGSEHELSENEEEBEBEBTEDDKDDDISD
                                                                          EKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPL
                                                                                                                                                  QGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVS
                                                                                                                                                                                                                          DNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEEEEEEEEDYEDDKDDDISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao QA;
VKONPLPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Goodrich RW, Liu C, Zhou P, Asundi V,
Xue AJ, Yang Y, Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 588; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP64928 standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-NOV-2001; 2001WO-US042950.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                       TFSEPG 408
                                                                                                                                                                                                                                                                                                                                        245 TESEPG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-590824/63
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                                                                                                                                                                                                                                                               185
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                                                                          223
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ABP64928

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cc nutritional sources or supplements. The proteins may be used to maintain and expand cell population in a totipotential or pluripotential state conseful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaccuticals or the development of bio-sensors. The colloporating disorders are useful for preventing, treating or ameliorating disorders involving aberrant protein expression or colloporating disorders involving aberrant protein expression or colloporating disorders, amenatopoietic disorders, central/peripheral nervous system diseases, mechanical and traumatic disorders, non-healing wounds, immune deficiencies and disorders, infectious diseases caused by conviral, bacterial or fungal infection, autoimmune disorders, allergic reactions and conditions, coagulation disorders, or cancer. The polymotactide sequences of the invention were assembled from ESTs isolated mainly by sequencing by hybridisation, and in some cases, captures obtained from one or more public databases. Note: The sequence data for this patent did not form part of the printed specification, but we will be published pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 QEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 EHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEH 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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100.0%; Pred. No. 4.9e-58;
tive 0; Mismatches 0;
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ADK65836 standard; protein; 91 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 VQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 QEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----LGLEHIWMRREPRQHLLSTGSLAEAESFSSLSTGSVLSPDGIDFSQDDEDDN 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     393 EDDKODDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERML-- 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ YQDEEV-- 132
                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                            16
           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      557 NTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLE-----ILIKDTLGLPVAGQ
                                                                                                                                                                                                                                                                                                                                            205 SSNGIGSGSGGYFTPDMSHSLSLAVVSEQVLLQEATTPN-----ELLYEMTPNSNAMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSF-PGKKITSRAAAPVCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461 SSGFGSSASGNSTTTSNQTS---GSAVRKSFGYQSAVENSQLSRLSSSAPTH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ------SETDOLTED-----STED-----CKDIENLE--SFTDVLDNEGALTSNWEQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---IEDFLPQTAV-----TQSVNFLLSPQAQGQDALVAPPMELLQQQQQNHQQLQVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 KTLQAEVPLSDCVQKASKPPSST----QIMVKTNMYHNEKVNFHVECKDYVKKAKVKINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
15.1%; Score 506; DB 4; Length 814;
Best Local Similarity 25.0%; Pred. No. 1.7e-29;
Matches 186; Conservative 94; Mismatches 211; Indels 254; Gaps
                                                                                                                                                                                                                                                                                                                     SVSGMDPPFGDAF---RSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL-
                                                                                                                                                                                                                                                                                                                                                                                                                    357 LPQLQTLLTLSQQQQSNSSSTSPYEIYHSTPQKPQQQQLSASFSPGSQASQSPLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 DIYCEDLIKYIKLISCDIWGIKEVDYL-----GLDDFSSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSEFVNQVLEKTAEGNPTGGLVGLR 633
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                                                                                                                                                                                                                 Sequence 814 AA;
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ADK65836

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a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary force of the involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
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                                                                                                                           angiogenesis inhibitor; angiogenesis stimulator; angiogenic index; gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449 MLRPSEWNRDTLPSNMYQKONGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer. Coronary artery disease, myocardial ischemia and/or arteriosclerosis.
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                                                                                                                   cardiant; vasotropic; antiarteriosclerotic;
                                                                                   Angiogenesis-differentially expressed protein #50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 434; DB 7;
Pred. No. 2.3e-25;
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100.0%; Pred. No. ....
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          Fan W,
                                                                                                                                                                                                                                                                                                                                                                                          (ORIG-) ORIGENE TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                07-FEB-2002; 2002US-00067482.
10-JUN-2002; 2002US-00164595.
16-AUG-2002; 2002US-0403649P.
03-JAN-2003; 2003US-0437746P.
                                                                                                                                                                                                                                                                                    07-FEB-2003; 2003WO-US003848
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                                                                                                                                                                                                                                                                                                                                                                                                                          Li X, Kovacs KF,
                                                          (first entry)
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                                                                                                                                                                                                                            WO2003066831-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 91 AA;
                                                                                                                                                                                                Homo sapiens
                                                          06-MAY-2004
                                                                                                                    cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sun Z,
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ADD46090 standard; protein; 712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Woolf C, D'urso D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP 308
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                               Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention discloses a composition comprising two or more isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 DEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 QTKKAAVPTP--AKKAAVTPG------KKAAATPAKKAVTPAKVVPTP---
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22.4%; Pred. No. 3.1e-06;
Live 60; Mismatches 171; Indels 140;
                                                                                                                                                                                                                                                                                                                                          Costigan M;
Rat Protein P13383, SEQ ID NO 7544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                                                                                                                                                          Befort K,
                                                                                                                                                                                                                      14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                      14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP.
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GENBANK; P13383.
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                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                                                                         FARB ) BAYER AG.
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or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also comprising the rovel polynucleotide, a host cell comprising the vector amethod for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially
398
                                                                                                                                                                                                                                                                                                                                                                                                                                                           456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 RDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVS 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 EPTTPFNLF------KSVAELKVAISELFAKN 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               517 EL-PLTARPRSRKEKNKLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQE 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 GKNAKKEDSDEDEDEEDEDDSDEDEDEEDEFEPPVVKGVKPAKAAPAAPASEDEDEEDDD
                                                                                                                                                                                                                                                                                            363 DVDDEDHDEGFGSEHELSENEEE--------EEEEEDYEDDKDD
                                                                                                                                                                                                                                                                                                                                                399 DISDIFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLIPSQQ--ERMLRPSEWN
                                                                                                                        309 GSLAAGESSSLSASTSVSDSSQXKEEHNYSLFVSDNLGEQPTKCSP-----EEDEEDEE
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expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of the polypeptides given in the pain and a pharmaceutical composition comprising the one or more pain and a pharmaceutical composition comprising the one or more polypeptides or thair antibodies. The polynuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (CMI)) in an animal (e.g. spin (e.g. spinal segmental nerve injury (SMI)) in an animal (e.g. spinal paperner of page of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the wipo int/pub/published_pct_sequences.
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Costigan M;

Befort K,

Woolf C, D'urso D,

GENBANK; AAA41732

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

(GEHO) GEN HOSPITAL CORP

(FARB) BAYER AG.

14-AUG-2002; 2002WO-US025765.

27-FEB-2003

Sequence 712 AA;

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305 EPITPFNLF-----KSVAELKVAISELFAKN 337
                                                                                                                                                                                 249 RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP 308
                                                                                                                                                                                                                                                                                                            309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP-----EEDBEDBE 362
                                                                                                                                                                                                                                                                                                                                    DVDDEDHDEGFGSEHELSENEEE---------EEEEEDYEDDKDD 398
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                                                                             129 DEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSS 188
                                                                                                                                                       189 KTLQAEVPLSDCVQXASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS 248
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Query Match 6.0%; Score 202; DB 7; Length 712;
Best Local Similarity 22.4%; Pred. No. 3.1e-06;
Matches 107; Conservative 60; Mismatches 171; Indels 140; Gaps
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Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung. Rat Protein AAA41732, SEQ ID NO 3693 ADE57828 standard; protein; 712 (first entry) Rattus norvegicus. MO2003016475-A2 29-JAN-2004 ADE57828 RESULT 10 ADE57828

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The invention discloses a composition comprising two or more insurance of laimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expression of a polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a compound that regulates the activity of one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the compound a method for identifying a compound sector in the polypeptides or their antibodies. The polynucleotide or the compound that composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that in the polypeptides or their antibodies. The polynucleotide or the compound that in the polypeptides or their antibodies. The polynucleotide or the compound that composition comprising the one or more injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed contraction which is differentially expressed during pain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pecification, a method for identifying a compound useful in treating pain and a pharmaceutical composition compressing the or more of the polypeptides given in the general pharmaceutical composition compressing the one or more of mother compound that antibodies or their antibodies or method for identifying a compound useful in treating pain and a pharmaceutical composition compressing the one or more of modulates its activity is useful for preparing a medicament for treating
                             DISDIFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQ--ERMLRPSEWN 456
                                                                                         457 RDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVS 516
                                                                                                           305 EPTTPFNLF------KSVAELKVAISELFAKN 337
DEDDDDDDE---EEEEEDDSEEEVMEITPAKGKKTPAKVVPVKAKSVAEEEEDDEDDEDE 252
                                                          253 EEDE--DEEDBEDDEDEEBEEEEPVKAAPGKRK-----KEMTKQKEAPEAKKQKIEGS 304
                                                                                                                                                                                                                                                                                                                                                                                 Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
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                                                                                                                                                                                                                                                                                                                          6.0%; Score 202; DB 7; Length 712;
22.4%; Pred. No. 3.1e-06;
tive 60; Mismatches 171; Indels 140;
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                 Query Match
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The present sequence is the Kaposi's sarcoma-associated herpesvirus, (KSHV) latency-associated nuclear antigen (LANA). KSHV is also known as Human Herpes Virus 8 (HHV8) and belongs to the rhadino virus, or gamma-2 herpes virus class. The LANA protein is necessary for the efficient persistence of rhadino virus DNA in mammalian cells. Persistent rhadino virus infection is implicated in a variety of diseases e.g. Kaposi's Sarcoma (KS). Primary Effusion Lymphona (PEL) and multicentric castleman's disease. In addition, KS is a common malignancy in HV patients. KSHV persists in host cells in a latent form. One of the few genes expressed from the latent viral DNA is LANA. Associates with coth human chromosomes and with the rhadino virus cis-acting element (RVCAE), thereby providing a tethering function: the KSHV DNA episome is "tied" to the host chromosomes. This allows the viral DNA to persist in the host cell. The present sequence may be used to screen and identify molecules that inhibit LANA interaction with RVCAE, thereby interfering with the latency cycle of this virus. Potential antiviral treatments for the above mentioned diseases may therefore be based on LANA deregulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIXVGSSSGGDTPPRQPPTSPISIGS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 PVCSSKTLOAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating or preventing a disease associated with rhodino virus infection in a mammal which includes Kaposi's Sarcoma and Primary Effusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.9%; Score 196.5; DB 3; Length 1162;
24.2%; Pred. No. 1.7e-05;
tive 52; Mismatches 145; Indels 103;
                                                                   550. .589
/note= "Gln, Glu, Pro, Arg-rich region"
590. .759
/note= "Gln, Glu, Asp-rich region"
760. .840
                                                   "Gln, Glu, Pro-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 12-SEP-2003 to standardise OS field)
                 note= "acidic repeat region"
                                                                                                                                                                    /note= "Gln, Glu-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaye KM;
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                                                                                                                                                                                                                                                                                                                       98US-00109422.
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/note= "ດາ
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Best Local Similarity 24.29
Matches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              (BALL/) BALLESTAS M E. (KAYE/) KAYE K M.
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N-PSDB; AAA30290.
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                                                                                                                                                                                                                                                                                   19-NOV-1999;
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                                                                                                                                                                                                                      The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed construction of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a colypoptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders convolving aberrant protein expression or biological activity. The colypoptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540 LKKKAQYEANKVKLW-GLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIK 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus; latency-associated nuclear antigen; LANA; gamma-2 herpes virus; Human herpes virus 61 HHV8; rhadino virus cis-acting element; RVCAE; Kaposi's sarcoma; primary effusion lymphoma; PEL; human immunodeficiency virus; HIV; multicentric Castleman's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "nuclear localisation signal, NLS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.0%; Score 200.5; DB 4; 73.0%; Pred. No. 4.4e-07; tive 2; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaposi's sarcoma-associated herpesvirus LANA.
                                                                                                                                                                                          Claim 20; SEQ ID NO 59634; 103pp; English.
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ID AAY96255 standard; protein; 1162 AA.
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(first entry)
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Best Local Similarity 73.0%
Matches 46; Conservative
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                                       WPI; 2001-639362/73
   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 160 AA;
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                                                           N-PSDB; AAS93462
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   Drmanac RT,
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SPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
                                                                             ----- 368
                                                                                                              369 HDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE----- 419
                                                                                                                                                                                                                 380 DDEEDDEEEDEEEDEEEDEEEDEEDDEDDEDNEDE-----EDDEEEDKKEDEEDGGDGN 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HHV8; detection; diagnosis; Kaposi's sarcoma; AIDS; immunogen; antigen.
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                                                                                                                                                                                                                                                                                                                         420 -VTSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSE 454
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                                                                             NYSLFVSDNLGEQPTKCSPEEDEEDEE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HHV8 ORF 73 protein, SEQ ID NO:21.
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(first entry)
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10-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
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                                                                                                                                                                                                                                                                                   124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA
                                                                                                                                                                                                                                                                                                                                        111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 PPPSQOTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNOAGED---NGDNEISKESQVDKDD
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                                                                                                                                                                                                                                                                                                                                                                                               184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK
                                                                                                                                                                                                                               Gaps
     method
the assays are that reproducible results are obtained and the methor suitable for rapid throughput and screening of samples economically. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                            Indels 103;
                                                                                                                                                                        Length 1162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of KSHV tethering protein LANA.
                                                                                                                                                                  Query Match 5.9%; Score 196.5; DB 3; Best Local Similarity 24.2%; Pred. No. 1.7e-05; Matches 96; Conservative 52; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 -VISISSRKRGKRRYFWEYSEQLIPSQQERMLRPSE 454
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N-PSDB; AAF82901.
                                                                                                                    Sequence 1162 AA;
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cc tethering provides a composition comprising nucleic acid, histone H1

Cc for tethering the nucleic acid to the histone H1 protein, where the

Cc tethering protein is LANA. The composition is useful in aiding the

Cc tethering protein is LANA. The composition is useful in aiding the

Cc for compounds which are agonistic or antagonistic for the tethering of

Cc viral proteins to histone H1 and DNA binding sites are useful for

Cc viral proteins to histone H1 and DNA binding sites are useful for

Cc viral proteins to histone H1 and DNA binding sites are useful for

Cc vereloping the method of viral transfer. The composition has applications

Cc opene therapy, including the treatment of multiple sclerosis,

Cc parkingon's disease, huntingon disease and diabetes. The present

C sequence represents the amino acid sequence of the Kaposi's sarcoma

associated herpesvirus (human herpesvirus 8) latency-associated nuclear

antigen (LANA), which acts as a tethering protein. (Updated on 06-NUG-

XX.

2003 to correct OS field.)
                     Disclosure; Fig 9B; 60pp; English
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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Sequence 1162 AA;

14; 111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162 184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237 238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285 209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268 286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335 269 SSPSEGSWGDDTAMLVILAEIAEEAŠKNEKECSENNQAGED---NGDNEISKESQVDKDD 325 336 NYSLFVSDNLGEQPTKCSPEEDEEDEE -----------------------------DVDDED 368 326 N-----DNXDDEEEQETDEEDBEEDDEEDDEEDDEEDDEEDDEE 379 369 HDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE----- 419 124 SSPYQDEEVISKTPTLAOLNSEDSQSVSDSLYYPDSLFSVKONPLPSSFPGKKITSRAAA 183 Query Match
5.9%; Score 196.5; DB 4; Length 1162;
Best Local Similarity 24.2%; Pred. No. 1.7e-05;
Matches 96; Conservative 52; Mismatches 145; Indels 103; Gaps 420 -VTSISSRKRGKRRYFWEYSEQLTPSQOERMLRPSE 454 셤 g ð g ઠ g ઠે 셤 ઠે g ઠે 8 ઠ

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Search completed: February 28, 2006, 08:45:04 Job time : 222.872 secs

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Sequence 75, App]
                                                                                                                                            (without alignments)
960.804 Million cell updates/sec
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Sequence 1904
Sequence 2651,
Sequence 8427,
                                                                                                                     February 28, 2006, 08:53:26; Search time 54.985 Seconds
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Sequence 2
Sequence 3
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3349
1 MPQPSVSGMDPPFGDAFRSH......TAEGNPTGGLVGLRIPTSKV
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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2: /cgn2 6/ptodata/1/iaa/6 COMB.pep:*
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4: /cgn2 6/ptodata/1/iaa/H COMB.pep:*
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US-08-714-741-41
US-08-714-134-2
US-08-935-855-22
US-10-104-047-251
US-09-949-016-8427
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Gapop 10.0 , Gapext 0.5
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US-09-241-333-3 US-09-248-796A-2062B US-09-047-026A-4 US-09-949-016-9676 US-09-949-016-9676 US-09-819-470-71 US-09-819-470-71 US-08-819-855-2 US-09-248-796A-24492 US-09-248-796A-24492 US-09-248-796A-24492 US-09-248-796A-24492 US-09-345-294-28 US-09-345-294-28 US-09-345-294-28 US-09-345-294-28 US-09-345-294-28 US-09-345-294-28 US-09-346-286-20 US-09-346-286-20 US-09-346-286-20 US-09-949-016-6265 US-09-949-016-6265	ALIGNMENTS	/10164595 ogies, Inc ted Angiogenesis Genes and : US/10/164,595 -06-10	<pre>%; Score 3349; DB 2; %; Pred. No. 3.7e-279; 0; Mismatches 0;</pre>	MPQBSVSGMDPPFGDAFRSHTFSEQTLANSIDPDFMYELDREMNYQONPRDNFL 	SLEDCKDIENLESFTDVLDNEGALTSNWEGWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL 	DDFSSPYQDBEVISKTPTLAQLNSEDSQSVSDSLYYPDSLF: 	AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV 	KINDVQOSRPLLSQIHTDAAKENTCYCGAVAKROEKKGMEPLQCHATPALPFKETOBLLL
4.9 4.8 4.8 4.8 4.8 4.8 4.8 4.8 4.8		tion US Technol Regula 103 R1 103 R2 103 R3 104 R2 105 R2 105 R3 105 R3 105 R3 105 R3	100.0%; Similarity 100.0%; 9; Conservative	MPQPSVSGMDPPFGDAF! 	SLEDCKDIENLESFTDVI 	DDFSSPYQDEEVISKTP' DDFSSPYQDEEVISKTP'	AAAPVCSSKTLQAEVPL. AAAPVCSSKTLQAEVPL.	KINPVQQSRPLLSQIHT
28 162.5 30 161.5 31 160.5 32 160.5 34 160.5 35 160.5 36 159 40 159 41 158 44 158		RESULT 1 US-10-164-595-44 Sequence 44, Application Patent No. 6657054 GENERAL INFORMATION: APPLICANT: OriGene TITLE OF INVENTION: Re- FILE REFERENCE: 1U 103 CURRENT APPLICATION NU CURRENT FILING DATE: NUMBER OF SEQ ID NOS: SOFTWARE: PATENTIN VET SEQ ID NO 44 LENGTH: 639 TYPE: PRT TYPE: PRT TYPE: PRT COGANISM: Homo sapien US-10-164-595-44	Query Match Best Local Si Matches 639,	9y 11	Oy 61 8	Qy 121 1 Db 121 1	Qy 181 Db 181	Oy 241 1 Db 241 1

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558 TEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLE---
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APPLICATION NUMBER: US/08/728,323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Cooper & Dunham LLP
1185 Avenue of the Americas
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                   610 SEFVNQVLEKTAEGNPTGGLVGLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Drosophila melanogaster US-09-270-767-57041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-09-270-767-57041
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LENGTH: 141
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COUNTRY:
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                                 421 TSISSRKRGKRRYFWEXSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
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APPLICANT: Origene Technologies, Inc
APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REPERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
SEQ ID NO 75
LENGTH: 91
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49.3%; Pred. No. 5.2e-20;
tive 22; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th 13.0%; Score 434; DB 2; Length 91 Similarity 100.0%; Pred. No. 9.3e-30; B3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 601 LGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLKIPTSKV 639
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Patent No. 6657054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Drosophila melanogaster
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Matches 71; Conservative
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; ORGANISM: Homo sapiens
US-10-164-595-75
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Best Local Similarity
Matches 83; Conserv
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US-10-164-595-75
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---ILIKDTLGLPVAGQT 609
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE PERERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 14; Gaps
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APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
APPLICANT: Moore, Parrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA TITLE OF INVENTION: Encoding Same And Uses Thereof NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
9.7%; Score 324; DB 2; L
Best Local Similarity 49.3%; Pred. No. 5.2e-20;
Matches 71; Conservative 22; Mismatches 37;
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US-09-410-399-2
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Query Match
                   Best Local
Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 SSPYQDEBVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
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APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Ballestas, Mary E.
APPLICANT: Raye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US 60/109,422
EARLIER APPLICATION NUMBER: US 60/109,422
RARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK
                                                                                                                                                                                                                                                                                                                                                           Indels 103; Gaps
                                                                                                                                                                                                                                                                                                                      Length 1162;
             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REFERENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELEPRAX: 212-278-0400
TELEPRAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 2: SEGUENCE CIRRACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                    Query Match 5.9%; Score 196.5; DB 1;
Best Local Similarity 24.2%; Pred. No. 1.2e-07;
Matches 96; Conservative 52; Mismatches 145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-298-568-2
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US-09-298-568-2
; Sequence 2, Application US/09298568
; Patent No. 6322792
                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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APPLICANT: Robertson, Erle S.
APPLICANT: Robertson, Erle S.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
TITLE OF INVENTION: OGENOMIC HOST DNA
FILE REPERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
SOFTWARE: PAtentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 ATPALPF -- KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
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                                                                                                             124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                                                                    111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
                                                                                                                                                                                                                                                            238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKROEKKGMEPLQ----GH 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 SSPSEGSWGDDTAMLVILAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
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                                                                                                                                                                                                                           PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK
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5.9%; Score 196.5; DB 2; Length 1162; 24.2%; Pred. No. 1.2e-07; ative 52; Mismatches 145; Indels 103;
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 NYSLFVSDNLGEOPTKCSPEEDEEDEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-410-399-2; Sequence 2, Application US/09410399; Patent No. 648289; GENERAL INFORMATION:
                                                              96; Conservative
                                   Similarity
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APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED mRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQ-----NPLPSSFPGK-KITSRAAA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.5%; Score 184; DB 1; L 20.2%; Pred. No. 7.4e-07; tive 69; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fasse, J. P.
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-5070
TELEPHONE: (617)542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 764 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 20.29
Matches 98; Conservative
                                                                                                                                                                                                                                                                     STREET: 225 Franklin S CITY: Boston STATE: MA COUNTRY: USA ZIP: 02110-2804 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-375-300-4
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APPLICANT: Kleff, Biliott D.
APPLICANT: Kleff, Biliott D.
APPLICANT: Kaye, Kenneth M.
THILG OF INVENTION: FRADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE TILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/894,273
CURRENT FILING DATE: 2001-06-28
PRIOR FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1162
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
CREAMISM: Kaposi's sarcoma-associated herpesvirus
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-- DVDDED 368
                                       124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED----NGDNEISKESQVDKDD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 HDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE----- 419
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                                                                                                                                      369 HDEGFGSEHELSENEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE
                                                                                                                                                                                                                                                                                                                        434 KTLSIQSSQQQQEPQQQE-PQQQEPQQQEPLQEPQQ 468
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NYSLFVSDNLGEQPTKCSPEEDEEDEE --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-894-273-2
; Sequence 2, Application US/09894273
; Patent No. 6756203
; GENERAL INFORMATION:
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Qy 418 KEVTSISSRKBGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAN 477 Db 622RDIEMKRMYEEYERKLKDEE	RESULT 11 PCT-US95-16930-4 Sequence 14 Application PC/TUS9516930 GENERAL INFORMATION: TITLE OF INVENTION: HETRROLOGOUS POLYPETIDE TITLE OF INVENTION: HETRROLOGOUS POLYPETIDE TITLE OF INVENTION: HETRROLOGOUS POLYPETIDE TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF TITLE OF INVENTION: PUNCTION IN THE ABSENCE OF TITLE OF INVENTION: PROCUCES: CORRESPONDENCE S: ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street Suite 3100 CITY: BOSTON STREET: AMA COUNTY: BOSTON STREET: PLOPPY disk COMPUTER: READABLE FORM: MEDIUM TYPE: TROPA COMPATIBLE COMPUTER: TREADABLE FORM: MEDIUM TYPE: TROPA COMPATIBLE COMPUTER: TREADABLE FORM: MEDIUM TYPE: TROPS/NS-DOS SOFTWARE: PALORY NOWBER: MEDICATION NUMBER: PCT/US95/16930 FILING DATE: 20-DEC-1995 FILING DAT	TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELERA: (617)542-5070 TELERA: (617)542-806 TELERA: 200154 TELERA: 200154 TELERA: 200154 TELERA: 200154 TELERA: 200154 TELERA: 617)542-806 TELERA: 200164 TELERA: 200164 TELERA: 617)542-806 TELERA: 617)64 TELERA: 617)64 TELERA: 617, 617, 617 TELERA: 617, 617 TELERA: 617, 617 TELERA: 617 TELERA: 617 TELERA: 617 TYPE: 617 TYPE: 617 TELERA: 61
Oy 556 LNTEYD 561 : Db 759 LKRSFD 764 RESULT 10 US-09-177-431-4 ; Sequence 4, Application US/09177431 ; Patent No. 6071700 ; Patent No. 6071700 ; Patent No. 6071700 ; Tarent No. 6071700 ; Title OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE ; TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MRNA DECAY FUNCTION ; NUMBER OF SEQUENCES: 18	CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CTTY: Boston STATE: MA CUNTRY: USA ZIP: 0210-2804 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE COMPUTER: FeatSEQ for Windows 95 SOFTWARE: FeatSEQ for Windows Version 2.0b SOFTWARE: FeatSEQ for Windows 95 SOFTWARE: FeatSEQ for Windows 95 SOFTWARE: FeatSEQ for Windows Version 2.0b SOFTWARE: FeatSEQ for Windows 95 SOFTWARE: FeatSEQ for Windows 95 SOFTWARE: FeatSEQ for Windows 95 SOFTWARE: APPLICATION DATE: FILMO DATE: FRICATION NUMBER: 08/955,472 FILMO DATE: REGISTRATION NUMBER: 07917/050001 TELECOMMUTCATION NUMBER: 07917/050001 TELECOMMUTCATION NUMBER: 07917/050001 TELECOMMUTCATION NUMBER: 07917/050001 TELEFAX: 617/542-9806 TELEFAX:	Query Match 5.5%; Score 184; DB 2; Length 764; Best Local Similarity 20.2%; Pred. No. 7.4e-07; 133 ISKTPTLAQLNSEDSQSVSDSLYPDSLFSVKQ. 160; Gaps 18; QY 133 ISKTPTLAQLNSEDSQSVSDSLYPDSLFSVKQ.

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133 ISKTPTLAQLMSEDSQSVSDSLYYPDSLFSVKQ------NPLPSSFPGK-KITSRAAA 183
                                                                                                                                                                                                                                     238 AKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQE 297
                                                                                                                                                                                                                                                                                                                                                                                            358 EEDEEDVODEDHDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDL 417
                                                                                                                                                                                                                                                                                                                298 LLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEED 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 KEVTSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAV 477
                                                                                                                                                        184 PVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKT-----NMYHNEKVNFHVECKDYVKK
                                                                                                                                                                                                                                                          478 KKSRRIDVEDLIPNPKKLLQIGNELRKLNKVISDLIPVSELPLIAR------PRSR
                                                                                                                 707 INNOPNPFYLNYSDP------PDNYFRIOLVTTILLNINRTPAAFTKKCKLLLR---
                                                                                                                                                                                               755 -PPEYYTFIKEQPL------PKETEFRVSSTFKKYENIFGNTK-----FER
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APPLICANT: Hacobson, Allan S.
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE PRODUCTION IN THE
TITLE OF INVENTION: ABSENCE OF NONSENSE-MEDIATED MENA DECAY FUNCTION
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                        Indels 160;
Length 1089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.5%; Score 184; DB 1; L 20.2%; Pred. No. 1.3e-06; tive 69; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/177,431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07917/050001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
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; Sequence 2. Application US/09177431
; Patent No. 6071700
; GENERAL INFORMATION:
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Query Match
Best Local Similarity 20.2%
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1084 LKRSFD 1089
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STATE:
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Batent No. 5679566

GENERAL INFORMATION:
APPLICANT: Feng, He
APPLICANT: Jacobson, Allan S.
TITLE OF INVENTION: THE ABSENCE OF NONSENSE-MEDIATED mRNA DECAY FUNCTION
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSES: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                    --ERKAEEELERQFQKAMQESIDARKSEKVVASKIPVISKPVSVQKPLLLKKSEEPSSS 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :| | :| | :| | 699 KETYEELSKPKKIAFTFLTKSGKKTQSRILQLPTDVKFVSDVLEEEEKLKTERNKIKKIV 758
      -----FER 468
                                            238 AKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQE 297
                                                                                 521
                                                                                                                     LLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPRED 357
                                                                                                                                                                                                   EEDEEDVODEDHDEGFGSEHELSENEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDL 417
                                                                                                                                                                                                                         418 KEVTSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAV 477
                                                                                                                                                                                                                                                                                                                       ----- 641
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                                                                                                                                                469 SENLVESASRLESILKSLNAIKSKODRVKGSSASIHNGKESAVPIES-----ITEDDE
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      430 -FFEYYTFIKEQPL------PKETEFRVSSTFKKYENIFGNTK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIF: 02110-2804
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OCREVITER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                     -----ERLIEMKRMYEEY------ERKLKDEE
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/046001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)542-8906
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APPLICATION NUMBER: US/08/375,300
FILING DATE: 20-JAN-1995
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
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STRANDEDNESS: not re:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKRSFD 764
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TELEX: 2
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Best Local Similarity 20.2%; Pred. No. 1.3e-06;
Matches 98; Conservative 69; Mismatches 159; Indels 160; Gaps
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GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL SCHOOL
TITLE OF INVENTION: HETEROLOGOUS POLYPEPTIDE
TITLE OF INVENTION: PRODUCTION IN THE ABSENCE OF
TITLE OF INVENTION: PUNCTION IN THE ABSENCE OF
TITLE OF INVENTION: PUNCTION
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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225 Franklin Street Suite 3100
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IBM PC compatible
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-9806
                                          TELEFAX: 617/542-9806
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1089 amino acids
TYPE: amino acids
TYPE: amino acids
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
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|084 LKRSFD 1089
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02110-2804
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CITY: Boston
STATE: MA
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Sequence 15197, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1089;
           UNEXALING SISIEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16930
FILING DATE: 27-DEC-1995
FILING DATE: 27-DEC-1995
FILING DATE: 27-DEC-1995
FILING DATE: 20-JAN-1995
ATORNEY/AGENT INFORMATION:
NAME: FREEE J. 962
REGISTRATION NUMBER: 32,983
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617)542-5070
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Best Local Similarity 20.2%; Pred. No. 1.3e-06;
Matches 98; Conservative 69; Mismatches 159;
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OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1089 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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US-09-248-796A-15197
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                                                                                                                                                                                                                                                                                                                             Query Match 5.3%; Score 176.5; DB 2; Length 428;
Best Local Similarity 21.7%; Pred. No. 1.4e-06;
Matches 103; Conservative 71; Mismatches 152; Indels 149; Gaps
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      FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: FOR DIAGNOSTICS AND THER FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 15197
                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: Candida albicans
US-09-248-796A-15197
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Search completed: February 28, 2006, 08:56:05 Job time : 56.235 secs

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US-10-717-665-44
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Sequence 31914, A
Sequence 75, Appl
                                                                                                                                    (without alignments)
1433.071 Million cell updates/sec
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                                                                                                                 February 28, 2006, 08:54:36; Search time 186.308 Seconds
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1 MPQPSVSGMDPPFGDAFRSH......TAEGNPTGGLVGLRIPTSKV
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
  GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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US-10-425-114-58474
US-10-128-714-8193
US-10-30-797-3328
US-10-504-582-158
US-10-369-493-3947
US-11-099-143-29151
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US-10-717-665-75
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US-09-894-273-2
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US-10-491-545A-20
US-10-374-763-40303
US-10-374-780A-522
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US-10-194-046-2
US-110-732-923-3319
US-110-483-505-3
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Gapop 10.0 , Gapext 0.5
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34710, A
71, Appl
72, Appl
71, Appl
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; Bublication No. US20050106579A1
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies, Inc
; TITLE OF INVENTION:
; CURRENT APPLICATION NUMBER: US/10/717,665
; CURRENT FILING DATE: 2003-11-21
; PRIOR PILING DATE: 2003-11-21
; PRIOR PILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; TANGENT OF 44.595
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100.0%; Pred. No. 3.1e-211;
ive 0; Mismatches 0;
US-11-013-684-7
US-10-369-493-22462
US-10-451-467A-388
US-09-839-479-21
US-10-376-537-21
US-10-376-537-21
US-10-489-740-176
US-10-702-148-21
US-10-732-923-3352
US-10-732-923-8311
US-10-218-137-21
US-11-097-143-15765
US-10-28-148-71
US-10-376-537-72
US-10-376-537-72
US-10-376-537-72
US-10-376-537-72
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Matches 639, Conservative
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357 LPQLQTLLTLSQQQQSNSSSTSPYEIYHSTPQKPQQQQLSASFSPGSQASQASPLTP---- 412
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                                                                                                                                                                                                                                                                                                      305 QEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDDV
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                                                                                 189 KTLQAEVPLSDCVQKASKPPSST----QIMVKTNMYHNEKVNFHVECKDYVKKAKVKINP
                                                                                                                                   -------PPPPHANRPQYQMVKSRNM-------QELIKKGFPMSSP
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Publication No. US20050106579A1
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
ITLLE OF INVENTION: RESPONDED A Majogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/717,665
CURRENT FILING DATE: 2003-11-21
PRIOR FILING DATE: 2002-06-10
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SOFTWARE: Patentin version 3.1
SEQ ID NO 75
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EXPRESSION OF 10,000 OR MORE
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                                                             TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
                                                                                                             TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
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; Publication No. US2005020858A1
; Publication No. US2005020858A1
; GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
: TITLE OF INVENTION: BARANS, FOR BETECTING EXP
TITLE OF INVENTION: ARRANS, FOR DETECTING EXP
TITLE OF INVENTION: BARANS, FOR DETECTING EXP
TITLE OF INVENTION: ARRANS, FOR DETECTING EXP
TITLE OF INVENTION: ARRANS, FOR DETECTING EXP
TITLE OF INVENTION: BARANS, FOR DETECTING EXP
TILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/161,93
PRIOR APPLICATION NUMBER: 60/161,93
PRIOR APPLICATION NUMBER: 60/115,693
PRIOR APPLICATION NUMBER: 60/115,693
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 1999-11-2
PRIOR FILING DATE: 2000-01-2
PRIOR APPLICATION NUMBER: 60/115,693
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US-11-097-143-31914
                                                                                                                421
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209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268
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209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIXVGSSSDGDTPPRQPPTSPISIGS 268
                                                                                                       269 SSPSEGSWGDDTAMLVILAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
                                                                                                                                                                                                380 DDERDDEEEDREEDEEEDEEEDEEEDDEEDDDEDNEDE-----EDDEEEDKKEDEEEDGGDGN 433
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                                                                                                                                                                        -----DVDDED 368
                                                                                                                                                                                                                                                                        369 HDEGFGSEHELSENEEEEEEEEDYEDDKODDISDTFSEPGYENDSVEDLKE----- 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Robertson, Erle S. APPLICANT: Robertson, Erle S. TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA TITLE OF INVENTION: to Genomic Host DNA FILE REFERENCE: UM-03778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ
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                                                                      286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH
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5.9%; Score 196.5; DB 4; Length 1162;
Best Local Similarity 24.2%; Pred, No. 0.00056;
Matches 96; Conservative co. william
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CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: US/09/410,399
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                           336 NYSLFVSDNLGEQPTKCSPEEDEEDEE-
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; Sequence 2.3 Application US/09894273
; Publication No. US20040037847A1
; GENERAL INFORMATION:
    APPLICANT: Rieff, Elilott D.
    APPLICANT: Kaye, Kenneth M.
    TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US 60/109,422
; PRIOR APPLICATION NUMBER: US 60/109,422
; NUMBER OF SEQ ID NOS: 3
; SEQ ID NOS: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 160;
                                            Sequence 59634, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: HYSRQ, Inc
; FILE BEPERENCE: 790C1P3/US
; CURRENT APPLICATION NOWEL NUCLEIC ACIDS AND POLYPEPTIDES;
CURRENT PILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR PILING DATE: 2000-03-31
; PRIOR PLILING DATE: 2000-03-31
; PRIOR PLILING DATE: 2000-03-31
; PRIOR PLILING DATE: 2000-03-31
; PRIOR SEQ ID NOS: 60736
; SOFTWARE: CUSTOM
; SEQ ID NO 59634
; LENGTH: 160
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Pred. No. 2.3e-05;
2; Mismatches 12;
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Best Local Similarity 73.0%;
Matches 46; Conservative
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CORGANISM: Homo sapiens
US-10-450-763-59634
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66 DTL 68
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 HDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE-
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Publication No. US20050108791A1
GENERAL INPORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR FILING DATE: 2003-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRLSS--
                                                         APPLICATE Robertson, Erle S.
TITLE OF INVENTION: LANA Viral Protein Binding Sites
FILE REPERENCE: UM-07142
CURRENT APPLICATION NUMBER: US/10/194,046
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: 09/410,399
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Kaposi's sarcoma-associated herpesvirus US-10-194-046-2
Sequence 2, Application US/10194046 Publication No. US20040248081A1 GENERAL INFORMATION:
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SEQ ID NO 3319
LENGTH: 1003
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                                                                                                                                                                                                                                                                                                                                                                                                 163 PPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ
                                                                                                                                                                          124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA
                                                                                                Gaps
                                                                                       87;
Length 1003
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APPLICANT: RICHARDSON, Thomas W.; WARREN, Bridget A.;
APPLICANT: RICHARDSON, Thomas W.; WARREN, Bridget A.;
APPLICANT: YUE, Henry, BAUGHN, Mariah R.;
APPLICANT: YUE, Henry, BAUGHN, Mariah R.;
APPLICANT: EMERLING, Brooke M.; LAL, Preeti G.;
APPLICANT: EMERLING, Brooke M.; LAL, Preeti G.;
APPLICANT: RAMKUWAR, Jayalaxmi; Li, Joana X.;
APPLICANT: BARKINGA, Jayalaxmi; Li, Joana X.;
APPLICANT: BURFORD, Neil; ELLIOTT, Vicki S.;
APPLICANT: SANJAWWALA, Madhusudan M.; LEE, Ernestine A.;
APPLICANT: BURFORD, Neil; ELLIOTT, Vicki S.;
APPLICANT: BOROWSKY, Mark L.; YAO, Monique G.;
APPLICANT: BOROWSKY, Mark L.; YAO, Monique G.;
APPLICANT: BOROWSKY, Mark L.; YAO, Monique G.;
APPLICANT: WALIA, Natinder K.; HRFALIA, April J. A.;
APPLICANT: WALIA, NATINGER: US/10/483,505
CURRENT FILING DATE: 2004-12-12
PRIOR APPLICATION NUMBER: US 60/305,104
PRIOR FILING DATE: 2001-07-12
PRIOR PILING DATE: 2001-07-12
PRIOR PILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
    Query Match 5.8%; Score 194.5; DB 5; Length Best Local Similarity 24.5%; Pred. No. 0.00063; Matches 94; Conservative 55; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 WE----YSEQLTPSQQERMLRPSE 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-483-505-3
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Query Match
Best Local Similarity 22.2%
Matches 106; Conservative
                                TYPE: PRT
ORGANISM: Candida albicans
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                                                           ; ORGANISM: Cand:
US-10-032-585-7386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2724
 SEQ ID NO 7386
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ORGANISM:
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Publication No. US20030180953A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
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                                                                                                                                                                                                                                                                                                                                                                                                                                  107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 -----SPTPD---GSERIGLEVDRRASRSSQSSKEEVNSEEYGSDHETGSSGSSDEQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 G-----EQPTKCSPEEDEEDVD-----DEDHDEGFGSEHELSENEEEEEEDYED 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 GNNTENBERGYVEEDVEEDVEEDAEEDBEVDEDGEB--EEFEEBEBEBEBEKYEED 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 -----CRIKKKAQYEANKVKLW----GLNTEYDNLLFVINSI-KQEI----VNRVQNPRD 583
                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 IKSNNHENVSLAKAKGVWSTL-PVNE------KKINLAFRSARSVILIFSVRESG
                                                                                                                                                                                                                                                                                                                                                         16 LDDILTEVPEQDDELYNPESEQDKWEKKGSKRKSDRM---ESTDTKRQKP---SVHSRQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 DYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPF
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                        120 LDDFSS--PYQDEEVISKTFTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKI
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253 DERDQKEEGNDYDTRSEASDSGSESVSFTDGSVRSGSGTDGSDEKKKERK------
                                                                                                                                                                                                                                           Query Match 5.7%; Score 189.5; DB 5; Length 735; Best Local Similarity 23.1%; Pred. No. 0.00089; Matches 134; Conservative 78; Mismatches 199; Indels 169;
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                                                                                                                                                                      ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7037554CD1
US-10-483-505-3
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PERL PROGRAM
SEQ ID NO 3
LENGTH: 735
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
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US-10-032-585-7386
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182 NNWAALRESLARIELPWSKHSFIEHQSITSADKTESEIK--DIYDDTERELAFYKQGLD- 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAFRACRLKKKAQYEANK---VKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 ----EISNDDDFQI-----ALEEATENNQKYGHGGSGSGDNKRKKPNSK 374
                                                                                                                                           314 GESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDE--DHDE
                                                                                                                                                                                                                                                                                                                                                                                                                                        372 GFGSEHELSENEEEEE-----EEEDYEDDKDDISDTFSEPGYENDSVEDLKEVTSISS
                                                                                                         197 LSDCVQKA-SKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV--KINPVQQSRPLLS
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                                                      69; Mismatches 150; Indels 152;
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                                                                                                                                                                                                                                                     61 --KSNTKKDDDDYQSEVLSKKEQRRLKKLQ------TKQQEE-----
DB 4; Length 427;
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                            Pred. No. 0.0021
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SEMERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NAKAGAWARA, AKIRA
APPLICANT: NAKAGAWARA, AKIRA
APPLICANT: SAKAKI, YOSHIYUKI
ITLE OF INVENTION: NOVEL HUMAN BMCCI GENE
FILE REFERENCE: 7388/80977
CURRENT APPLICATION NUMBER: US/10/487,593
CURRENT FILING DATE: 2004-02-24
FRIOR APPLICATION NUMBER: PCT/JF02/08520
FRIOR APPLICATION NUMBER: PCT/JF02/08520
FRIOR APPLICATION NUMBER: DCT/JF02/08520
FRIOR APPLICATION NUMBER: DCT/JF02/08520
FRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PALCHIN OF: 3.2
  5.3%; Score 179; 22.2%; Pred. No. 0.
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FILE REFERENCE: 03495.0166-01000
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LENGIH: 707
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Best Local
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139 PAPMASGOSQOSSHSADYSPADDFFPNSDLSEGOLPAGPEGLDGMGTNMSNYSSSSLLSG 198
                                                                                                                                                                                 317 QESVFQSPESWKEHKPSSIDRRASDSVFQPKSLEFTKGGPWESEF-------GQPELG
                                                  604 LDTNYSTSDSYTSPTFAGD---EKETEHKPPAKEEGFESKDGNSTAEETDIPPOSLOOSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       816 --WGLEYQEANQVDWELPASDEHTKDSAPSEHHTLN-----EKSGGLIANSI--WD
                                                                                               ---ALTSNWEQWDTYCEDLTK-----YTKLTSCDIWGTKEVDYLGLDDFSSPYO
                                                                                                                                                                                                                                                           SNDIQDKNEESLPFQNLPMEKSPLPNTSPQGTNHLIEDFASLWHSGRSPTAMPEPWGNPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 YENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLT---PSQQERMLRPSE---WNR----D
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                                                                                                                                                               DEEVISKTPTLAQLN-SEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCS
                                                                                                                                                                                                                             SKTLQ----AEVPLSDC-VQKASKP---PSSTQIMVK--TNMYHNEK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Hovanessian, Ara
APPLICANT: Arablebaut, Christian
APPLICANT: Jacotot, Etienne
APPLICANT: Muller, Sylviane
APPLICANT: Muller, Sylviane
APPLICANT: Guichard, Gan-Paul
APPLICANT: Guichard, Giles
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USES.
                              SDPDFMYELDRE-MNYQQNPRDNF---LSLEDCKDIENLESFTDVLDNEG
                                                                                                                                                                                                                                                                                            ------VNFHVECKDYVKKAKVKINPVQQSRPLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : : | : | : | |: | : 863 SVMRDKDMSSFMLPGSSHITDSEQRELPPEIPSHSANVKDTHSPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/09825886 Publication No. US20020076693A1
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US-09-825-886-22
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APPLICANT: HOVANESSIAN, ARA G.
APPLICANT: HOVANESSIAN, ARA G.
APPLICANT: HOVANESSIAN, JEAN-PAUL
TITLE OF INVENTION: INHIBITION OF VIRUS ANCHORAGE BY RGG DOMAIN OF A CELL SURFACE-
TITLE OF INVENTION: THERAPEUTIC USES THEREOF BY INHIBITION OF MICROORGANISM OR
TITLE OF INVENTION: PROTEIN LIGAND BINDING TO THE CELL-SURFACE-EXPRESSED PROTEIN
FILE REPERBENCE: 03495.026.0000
CURRENT APPLICATION NUMBER: US/10/384,569
CURRENT APPLICATION NUMBER: US/33,371
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CURRENT APPLICATION NUMBER: US/09/825,886
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: 09/393,302
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: PCT/EP98/01409
PRIOR FILING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 32
SOFFWARE: PatentIn Ver. 2.1
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US-09-825-886-22
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405 TQDEL 409
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TYPE: PRT
ORGANISM: Homo sapiens
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405 TQDEL 409
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US-10-400-083-19
Sequence 19, Application US/10400083
Publication No. US20040186056A1
Publication No. US20040186056A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erki
APPLICANT: Christian, Sven
TITLE OF INVENTION: HMR012 Peptides and Related Molecules
TITLE OF INVENTION: HMR012 Peptides and Related Molecules
TITLE OF INVENTION: HMR012 Peptides
FILE REFERENCE: P-LJ 5662
CURRENT FILING DATE: 2002-09
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 707

"WALL ELENGTH: 707
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 PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION WUMBER: 60/397,600
PRIOR FILING DATE: 2002-07-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PALENLIN Ver. 2.1
SEQ ID NO 3
LENGTH: 707
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ORGANISM: Homo sapiens
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:||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|: :||: :||: :||: :||: :||: :||: :||: :||: :|: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :|:
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APPLICANT: Liao, X. Charlene
APPLICANT: Liao, X. Charlene
APPLICANT: Mauda, Esteban
APPLICANT: Manda, Esteban
APPLICANT: Aborde, Horan
APPLICANT: Zhao, Haoran
APPLICANT: Zhao, Haoran
APPLICANT: Rigel Pharmaceuticals, Inc.
CURRENT REFERENCE: 021044-000330US
CURRENT PLILNG DATE: 2001-00-03
PRIOR PRICATION NUMBER: US 60/327,212
PRIOR PLILNG DATE: 2001-10-03
PRIOR FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 96
SEGFWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                             129 DEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSS
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Ouery Match 5.2%; Score 174; DB 4; Length 707;
Best Local Similarity 20.4%; Pred. No. 0.0088;
Matches 99; Conservative 76; Mismatches 162; Indels 148;
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                                                                                                                                                                                                     129 DEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSS 188
                                                                                                                        189 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS 248
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Sequence 2, Applisequence 293, Appl Sequence 292, Appl Sequence 2, Applisequence 49, Appl Sequence 169, Appl Sequence 169, Appl Sequence 107, Appl Sequence 107, Appl Sequence 305, Appl Sequence 434, Appl Sequence 288, Appl Sequence 288, Appl Sequence 288, Appl
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1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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8: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-124-368A-305
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US-11-124-368A-306
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	Sequence 2, Appli	Sequence 2964, Ap	Sequence 1120, Ap	Sequence 14, Appl	Sequence 415, App	Sequence 28, Appl	Sequence 29, Appl	Sequence 2050, Ap	Sequence 2755, Ap	Sequence 950, App	Seguence 968, App	970,	Sequence 10232, A	Seguence 1039, Ap	Seguence 14, Appl	Sequence 8, Appli	Sequence 962, App	Seguence 958, App	Seguence 960, App	
US-10-821-234-905	US-11-128-572-2	US-10-793-626-2964	US-10-821-234-1120	US-10-530-340-14	US-11-024-959-415	US-11-135-855-28	US-11-135-855-29	US-11-072-512-2050	US-11-072-512-2755	US-10-453-372-950	US-10-453-372-968	US-10-453-372-970	US-11-098-686-10232	US-10-821-234-1039	US-11-241-056-14	US-10-528-031-8	US-10-453-372-962	US-10-453-372-958	US-10-453-372-960	
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ALIGNMENTS

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pplication US/11072512 US20060029945A1 TON: TON: TAKAO TIYAWA, TOMOYASU UKI, TETSUJI TAMATO, UNIVI TON: THOOYUKI TI, SHIZUKO THROYUKI TI, SHIZUKO TON: TON: TON: TON: TON: TON: TON: TON	21.9%; Pred. No. 0.0029; vative 58; Mismatches 109;	276 KKGMEPLQCHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH	336 NYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHE
11. 0.72-512-2651 12.072-512-2651 2010-6251, Applica Application No. US2006 ENERAL INFORMATION THE STATE OF	al Sim: 74;	276 KK 86 KK	336 NY
RESULT 1 US-11-072-2651 US-11-072-512-2651 Sequence 2651, Appli Publication No. US20 CENERAL INFORMATION: APPLICANT: SUGIVA, APPLICANT: WAKAWAT APPLICANT: SATO, H APPLICANT: ISONO, APPLICANT: ISONO, APPLICANT: ISONO, APPLICANT: ISONO, APPLICANT: ISONO, APPLICANT: SEKI, N APPLICANT: RASURO, APPLICANT: NAGAL, APPLICANT: NAGAL, APPLICANT: NAGAL, APPLICANT: NAGAL, APPLICANT: NAGAL, APPLICANT: NAGAL, APPLICANT: NAGALAN APPLICANT: NAGALAN APPLICANT: NAGALAN APPLICANT: NAGALAN APPLICANT: MASURO, APPLICANT: MASURO, APPLICANT: MASURO, APPLICANT: MASURO, APPLICANT: NAGALAN SURRENT FILING DATE: PRIOR APPLICATION N PRIOR FILING DATE: NUMBER OF SEQ ID NG SOFTWARE: PATENTING DATE: NUMBER OF SEQ ID NG SOFTWARE: P	Best Local Similarity Matches 74; Conser	oy Op	δ

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APPLICANT: INSTITUT PASTEUR
APPLICANT: DRUILHE, PIERRE
TITLE OF INVENTION: IDENTIFICATION OF A CONSERVED REGION OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: MSP3 TARGETED BY BIOLOGICALLY ACTIVE ANTIBODIES
FILE REFERENCE: 275601US0
CURRENT APPLICATION NUMBER: US/11/189,817
CURRENT PILING DATE: 2005-07-27
PRIOR FILING DATE: 2005-07-37
PRIOR FILING DATE: 2004-08-03
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                                                                                                                                                 256 KRKKEMA----KQKAAPEAKKQKVEGTEPTTAFNLFVGNLNFNKSAPELKTGISDVFAK 310
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DEDEDEDEDEDE EPAAMKAAAAPASEDEDDEDDEDDEDDDE EDDSEERAMETTPAKG 195
                                                                                                                           467
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                                                                        196 KKAAKVVPVKAKNVAEDEDEEEDDEDEDDDEDDEDDEEEEEEEEEEFVKEAPG
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                                                                                                                          RKRGKRRYFWEYSEQLIPSQOERMLRPSE------WNRD-----TLPSNMYQK
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1 Similarity 20.9%; Pred. No. 0.0016;
82; Conservative 61; Mismatches 146; Indels 104; Gaps
                                                                                                                                                                                                                                                                                          516 SELPLTARPRSRKEKNKLAFRACRLKKKRAQYEANKVKL 553
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Publication No. US20060030006A1
GENERAL INFORMATION:
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US-11-189-817-2
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SOFTWARE: Patentin version 3.3
SEQ ID NO 2
LENGTH: 354
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APPLICANT: Statens Serum Institut
TITLE OF INVENTION: Vaccines comprising chimeric malaria proteins derived from Plasmoc
TITLE OF INVENTION: falciparum
FILE REFERENCE: 15007dk
CURRENT APPLICATION NUMBER: US/11/128,660
CURRENT FILING DATE: 2005-05-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SQIPSLDL----KEPTNEDILPNHNPLENIKQSESEIN-HVQDHA 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ISKTPTLAQLNS-EDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKIT 178
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4.7%; Score 157.5; DB 7; Length 651;
Best Local Similarity 18.4%; Pred. No. 0.0076;
Matches 99; Conservative 99; Mismatches 171; Indels 169;
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TITLE OF INVENTION: Human BMP2 Inducible Kinases
FILE REFERENCE: 004974.01015
CURRENT APPLICATION NUMBER: US/10/509,422
CURRENT FILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: PCT/EF03/080825
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Sequence 1, Application US/11128660
Publication No. US20060024324A1
GENERAL INFORMATION:
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Publication No. US20050244825A1
GENERAL INFORMATION:
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Query Match
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APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CLO01519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
                                                                                                                                                                                                                                     Query Match
4.6%; Score 155; DB 6; Length 1168;
Best Local Similarity 18.8%; Pred. No. 0.023;
Matches 117; Conservative 81; Mismatches 189; Indels 236;
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PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 60/367,512
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1168
TYPE: PRT
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US-10-509-422-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 KELDLSELDDPDSAYLQEARLKRKLIRLFGRLCEL--KDCSSLTGRVIEQRIPYRGTRYP
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Polymorphisms Associated with
FILE REFERENCE: CLOOL519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR PILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-06-50
PRIOR FILING DATE: 2004-06-50
PRIOR FILING DATE: 2004-06-50
PRIOR FILING DATE: 2004-06-09
SOFFWARE: PastSEQ ID NOS: 34460
SOFFWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%; Score 154; DB 7; Length 740;
22.0%; Pred. No. 0.015;
tive 63; Mismatches 162; Indels 130;
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                  PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: PASICE OF Windows Version 4.0
SEQ ID NO 293
LENGTH: 740
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APPLICANT: Michele Cargill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 ----VSPSLLSEEPLAPSS---
2005-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 22.0 Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
   CURRENT FILING DATE:
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US-11-124-367A-292
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Brown, Eugene
APPLICANT: Liu, wei
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: CANCERS
TILLE REPERENCE: AM10.1079 (031896-010000)
CURRENT APPLICATION NUMBER: US/10/770,726
CURRENT FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 48640
SOFTWARE: Patentin version 3.2
                                                                             24;
                                                                                                                                                                                             181 AAAPVCSS----KTLQAEVPLSDCVOKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440
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                                                                                 Gaps
Query Match
4.4%; Score 147.5; DB 6; Length 1618;
Best Local Similarity 19.9%; Pred. No. 0.1;
Matches 116; Conservative 90; Mismatches 204; Indels 173;
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20.2%; Pred. No. 0.056;
tive 80; Mismatches 214;
                                                                                                                                                                                                                                                                                                                                                                379 ARTPILASTPIPPTPOAPSPAVDAEIRAODAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 DDKDDDISDTFSE-PGYENDSVEDLKEVT----
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; Sequence 49, Application US/10770726
; Publication No. US20050266409A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                594 EILIK---
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APPLICANT: Zulewski, Hendrik
APPLICANT: Zulewski, Hendrik
APPLICANT: Zulewski, Hendrik
APPLICANT: Zulewski, Hendrik
APPLICANT: Zulewski, Hendrik
APPLICANT: Zulewski, Hendrik
APPLICANT: Vallejo, Maxio
TITLE OF INVENTION: METHOD OF TRANSPLANTING IN A MAMMAL AND TREATING DIABETES MELLITU
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
TITLE OF INVENTION: A NESTIN-POSITIVE PANCREATIC STEM CELL
TITLE OF INVENTION: A NUMBER: US 09/731,255
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 1999-12-06
PRIOR PELING DATE: 2000-16-28
PRIOR PELING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-28
PRIOR PELING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PATCHTIN VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TCYCGAVAKRQE---KKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAA- 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488 EQMQEGQEDDEEEDEEEAAAGKDGDKSPMSSLQISNEKNLEPGKQISRSSGEQQNKGRI 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :: :: | | : :: | | : :: | | :: :: | | :: | | :: | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | ::
                                                                                                                                                                                                                                                                                                                                   113 KEVDYLGLDDFSSPYODE----EVISKTPTLAQLNSEDSQSVSDSLY-----YP
                                                                                                                                                                                                                                                                                                                                                                                                         228 KELDLSELDDPDSAYLQEARLKRKLIRLFGRLCEL--KDCSSLTGRVIEQRIPYRGTRYP
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                         4.6%; Score 154; DB 7; Length 760;
22.0%; Pred. No. 0.015;
tive 63; Mismatches 162; Indels 130;
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                                                                                                                                                                                         Query Match
Best Local Similarity 22.09
Matches 100, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapiens
US-10-984-645-2
              ; LENGTH: 760
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --NEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSE 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 AAECAQEAE------PPKSEESFRSREAEEGQEGQDAMSRAKANWIRAFNKVRMQLQ 476
                                                                                                                                                                                                                                                                                             167 LP------VPSSQCCNWNYFGWGEQNDDPDSA-VDDRDSDY 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------PSEPR--ALSP----TGSSRYASSGELSQGSSQLSEDFDPDEH 284
                                                                              DY--LGLD-DFSSPYQ--DEEVISKTPTLAQLNS---EDSQSVSDSLYYPDSLFSVKQNP 167
                                                                                                                                                                                                                                                LPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCVQ-----KASKPPSSTQIMVKTNMY 220
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                                                                                                                                                                                                                                                                                                                                                                                              201 RSETSNSIPPPYYTTSQPNASVHQYSVRP----PPLGSR------ESYSDSMHSYEE
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                                                                                                                                                                                                 117 TFHRILLDAHFELPLDIPEEEARYWAKKLEQLNAMRDQDEYSFQDQ------QDKP
                                                                                                                                                                                                                                                                                                                                                    221 HNEKVN-----FHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQE
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                                               ------EDLTKYTK--LTSCDIWGTKEV
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4.3%; Score 144; DB 6; Length 1404;
Best Local Similarity 19.8%; Pred. No. 0.14;
Matches 141; Conservative 132; Mismatches 268; Indels 172;
25 TLKVQNVKSTTIAVRGSQPSWEQDFMFEINR------LDLGLTVE---
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US-10-878-556A-169
US-10-878-556A-169
Publication No. US20050266399A1
GENERAL INFORMATION:
APPLICANT: HOFfmann La-Roche Inc.
TITLE OF INVENTION: HCV regulated protein expression; FILE REFERENCE: 21762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 GLPV----AGQTS-----EFVNQVLEKTAE 622
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; DATABASE ENTRY DATE: 2003-04-22
US-10-878-556A-169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/878,556A CURRENT FILING DATE: 2004-06-28 NUMBER OF SEG ID NOS: 199
SOFTWARE: Parentin version 3.1
                                                    77 VLDNEGALTSNWEQWDTYC----
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PUBLICATION INFORMATION;
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LENGTH: 1404
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APPLICANT: ROSENMUND, Christian
APPLICANT: BROSE, Nils
APPLICANT: RHEE, Jeong-Seop
APPLICANT: RETTIG, Jens
APPLICANT: ANdrea
APPLICANT: ASHERY, Uri
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APPLICANT: UNGE, Harald
ATITLE OF INVENTION: UNC-13 IN THE MODULATION OF NEUROTRANSMISSION AND SECRETION EVENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 EEEEEEETGSN-SEEASEQSAEEVSEEEMSE----SRFDR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 DSGESEBAREEVGEGTPOSSALTEGDYV-----PDSPALSP----IELKQELPKYLPA 428
                                  221
                                                                                                                                                                                                                                                                          166 DRLEQLERKRERERKWREQQKEQREQKERERRAEERRKEREARREVSAHHRTWREDYSDK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 -LLSDLQDISDSERKTSSAESSSAESGSGSEEEEEEEEEEEGSTSE----ESEEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 MLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKV 508
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                                                                                                                                                                                                                                                                                                                                    286 -----ATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYS 338
                                                                                                                                                                                                                                                                                                                                                                                   226 VKASHWSRSPPRPPRERFEL----GDGR-KPGEARPARAQKPAQLKEEKMEERD-- 274
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                                                                              53 LRDH--RMEITIR-NSPYRREDSMEDRGEEDDSL--AIKPPQ--OMSRKEKVHHRKDEKR
                                                                                                                                                                    106 KEKRRHRSHSAEGGKHARVKEKEREHERRKRHREEQDKARREWERGKRREMAREHSRRER
                                                                                                                                                                                                                                                                                                                                                                                                                                     339 LFVSD--NLGEQPTKCSPEED-----EDEEDVDDEDHDEGFGSEHELSENEEEEE
                                  168 LPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYH-----
                                                                                                                                  -----KKAKVKINPVQQSR
                                                                                                                                                                                                                                      250 PLLSQIHTDAAKENTC-----YGGAVAKRQEKKGMEPLQGH------
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4.3%; Score 145.5; DB 6; Length
Best Local Similarity 20.4%; Pred. No. 0.15;
Matches 142; Conservative 87; Mismatches 208; Indels
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CURRENT FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: PCT/EP02/12072
PRIOR APPLICATION NUMBER: EP 01 12 6235.9
PRIOR APPLICATION NUMBER: EP 01 12 6235.9
PRIOR PILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 12
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SEQ ID NO 3
LENGTH: 1735
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                                                                                                                                                                                                                                                                                                                                                                                 TSRA----AAPVCSSKTLQAEVPL-SDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECK 232
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                                                                                                    ESFTDVLDNEGALTSNWE---QWDTYCEDLTKYTKLTSCDIWGTKEVDYL--GLDDFSSP 126
                                                                                                                                                                    ---TSVNELNSQLNESKEKVSQLDIQIKAKTEL--LLSAEAAKTAQRADLQNHLDTAQNA 668
                                                                                                                                                                                                                                            127 YQD--EEVISKTPTLAQLNS--EDSQSVSDSL----YYPDSLFSVKQNPLPSSFPGKKI 177
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE IDENTIFICATION OF
TITLE OF INVENTION: PROPERIORS IN VERTEBRATE CELLS
TITLE OF INVENTION: PROPERIOR INTERACTIONS IN VERTEBRATE CELLS
CURRENT FILE REPERBUGE: HAV-056.25
CURRENT APPLICATION NUMBER: US/10/475,204
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/US02/13008
PRIOR PILING DATE: 2003-09-27
PRIOR PILING DATE: 2003-09-27
NUMBER OF SEQ ID NOS: 35
SOFTHARE: PATENTIN VEY: 2.1
SSOFID NO 34
LENGTH: 943
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1162 IQQKLELQGKADSLKAAVEQEKRNQQILKD----QVKKEEEEELKKEFIEKEAK 1210
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Score 142; DB 6; Length 943; Pred. No. 0.12;
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Publication No. US20050277116A1
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; ORGANISM: Homo sapiens
US-10-475-204-34
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                                                                                                                                                                                                                                                                                                               280 EPLOGHATPALP------PKETQELLLS----PLPQEGPGSLAAGESSSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                         231 CKDYVKKAKVKINPVQOSRPLLS------QIHTDAAKE-NTCYCGAVAKROEKKGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SDIFSEPGYE--NDSVEDLKEVTSISSRKRG-----KRRYFWEYSEQLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 DEFQRNSDRNMEEHEEMGNDCVSK-KQMPPVGSKKSSTRKDKEESKKKRFSSESKNKLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          511 EEVTSTVTKSRRISRRPSDWWVVKSEESPVYSNSSVRNELPMHH-----NSSRK-----
                                                                                                                                                                                                                                                                 178 TSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNF-----HVE
71; Mismatches 147; Indels 168; Gaps
                                                                                                                                            ## STRING PATE: 100-01-01

## APPLICANT: Mezes et al.

## TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
## TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
## TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
## TITLE OF INVENTION: DATE: 2005-02-08

## CURRENT FILING DATE: 2005-02-08

## PRIOR APPLICATION NUMBER: 60/261,018

## PRIOR APPLICATION NUMBER: 60/261,013

## PRIOR APPLICATION NUMBER: 60/261,013

## PRIOR PILING DATE: 2001-01-11

## PRIOR PILING DATE: 2001-01-11

## PRIOR PILING DATE: 2001-01-11

## PRIOR APPLICATION NUMBER: 60/261,026

## PRIOR APPLICATION NUMBER: 60/261,029

## PRIOR APPLICATION NUMBER: 60/261,029

## PRIOR APPLICATION NUMBER: 60/261,029

## PRIOR PILING DATE: 2001-01-11

## PRIOR PILING DATE: 2001-08-17

## PRIOR PILING DATE: 2002-01-11

## PRIOR PILING DATE: 2001-08-17

## PRIOR PILING DATE: 2001-08-17

## PRIOR PILING DATE: 2001-08-17

## PRIOR PILING DATE: 2002-01-11

## PRIOR PILING DATE: 2001-08-17

## PRIOR PILING DATE: 2002-01-11

## PRIOR PILING DATE: 2002-08-17

## PRIOR PILING DATE: 2002-08-17

## PRIOR PILING DATE: 2002-08-17

## PRIOR PILING DATE: 2001-08-17

## PRIOR PILING DATE: 2002-08-17

## PRIOR PILING DATE: 2001-08-17

## PRIOR PILING DATE: 2001-08-17
                                                                                     131 EVISK-TP---TLAQLNSEDSQSVSDSLYY---
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Publication No. US20060013813A1
GENERAL INFORMATION:
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560 --STKKTNQSSKNIRK 573
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; ORGANISM: Rattus norvegicus
US-11-054-281-107
         Matches 110; Conservative
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; Sequence 305, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US 60/568,845
; PRIOR PILING DATE: 2004-05-07
; PRIOR PILING DATE: 2004-05-07
; PRIOR PILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTHARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2039 EPLAVSKLTRTSGETTQTHTEPTGDSKSİKAFKE------SPKQILDPAASVTGSR 2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 DLTKYTKLT-----SCDIWGTKEVDYLGLDDFSSPYQD-EEVISKTPTL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|| |: | ||| :| || :| || :| ||| :| ||| :| ||| :| ||| :| ||| :| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
: | : : | : : | 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                :| : : : | | : : : : | 467 PSAKESASQHITEEEDDDPDVYY---FESDHVALKHNKDYQRLLQTIAVLEAQRSQAVQD 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----IGNELRKIN-----KVISDLTPVSELPLTARPRS----RKEKNK 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GFVEKLQKKADIG--LPYPQRVVQ 561
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                                                                                                                                                                                                                                                 NYS-----LFVSDNLGEQPTKCSPEEDEEDV--DDEDH-DEGFG---SEHELSENE-
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                                                                                                       G--HATPALPFKETQELLLSPLPQEGPGSL-----AAGESSSLSASTSVSDSSQKKEEH
                                                                                                                                                     350 GEPEPSPVLDCVSAQMMSLSE-PQEHRYTLRTSPRRAAPTRGSPTKNSSPYRENGGFEEN
                                                                                                                                                                                                                                                                                               409 NLSPNETNATVSDNVSQSPT--NPGEISQNEKGICCDSQNNGSEGVSKPPSEARLNIGHL
                                                                                                                                                                                                                                                                                                                                                                                                  384 -EEEEEEEDYEDDKDDDISDTFSEPGYENDSV-----EDLKEVTSISSRKRGKRYFWEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 SEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQ
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524 LESLGRHQREALKNPI-----
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Best Local Similarity 19.9%
Matches 131; Conservative
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CORGANISM: Homo sapiens
US-11-124-368A-305
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APPLICANT: Jacob, Kenneth
APPLICANT: Jacob, Kenneth
APPLICANT: Jacob, John M
APPLICANT: Avelicant Racie, Lisa A
APPLICANT: Racie, Lisa A
APPLICANT: Racie, Lisa A
APPLICANT: Tacacy, David
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766, 000101.10;
CURRENT APPLICATION NUMBER: US/10/689,742;
CURRENT FILING DATE: 2003-10-22
PRIOR APPLICATION NUMBER: 09/746,783
PRIOR PLILNG DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patent In version 3.2
SEG ID NO 142
LENGTH: 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245
                                                                                    16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 NEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGLDDFSSPYQDEEVISKTPTL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 AQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSSKTLQAEVPLSD 199
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                                                                                                                                                                                                                                                                                                                                                    293 KETOELLLSPLP-----QEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         403 TFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNR--DTL 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 NSSDPDFMYELDREMNYQQ-----NPRD-----NFLSLEDC--KDIENLESFTDVLD 79
                                                                                                                                                                                                                              86
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                                                                                                                                                                                                   196 DLDNEENELEELEERVEARKKTTEKQQSQNLFLLWS-KLT----DRLWFKSSYSRXSSTL
                                                                                                                                                         250 PLLSQIHTDAAKENTCYC-----GAVAK----ROEKKGMEPLOGHATPALPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 NLGEQPTKCSPEEDEEDVDDEDHDEGFGSEHELSENEEEE-REEEDYEDDKDDDISD
                                                                                    74; Gaps
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   Query Match 4.2%; Score 142; DB 7; Length 1229; Best Local Similarity 24.7%; Pred. No. 0.16; Matches 67; Conservative 47; Mismatches 83; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.2%; Score 140.5; DB 6; Length 9 Best Local Similarity 20.2%; Pred. No. 0.14; Matches 142; Conservative 109; Mismatches 227; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PSNMYQKNGLHHGKYAVKKSRRTDVEDL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 LVETRNLYGVVG-----AESRSAPVEHL 273
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Publication No. US20050250180Al
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                                                                                                                                                2240 -----SLTAGKATKIPCESPPLEVVDTTASTKRHLRTRVQKVQVKEEPSAVKFTQTSG 2292
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                       ETTDADKEPAGE---DKGIKALKESAKOTPAPAASVTGSRRRPRAPRESAQAIEDLAGFK 2349
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                                                                    SSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQ 246
                                                                                                                                      247 QS----RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSP 302
                                                                                                                                                                                                           303 LPQEGPGSLAAGESSSL---SASTSVSDSSQKKEEHNYSLFVSDNLGEQP----TKCSP 354
                                                                                                                                                                                                                                                                               -----GSEHELSENEEEEEEDYEDDK 396
                                                                                                                                                                                                                                                                                                                                                DDDISDTFSEPGYENDSVEDLK------EVTSISSRKRGKRRYFWEYSEQLTPS 444
                                                                                                                                                                                                                                                                                                                                                                                                                   445 QOERMIRPSEWNRDTLPSNMYQKNGLHHGK----YAVKKSRRTDVEDLTPN-----PKK 494
140 AQLNS--EDSQSVSDSLYYPDSLFSV------KQNPLPSSFPGKKITSRAAAPVC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 433, Application US/11124367A

Publication No. US20060024700A1

Sequence 433, Application US/11124367A

Publication No. US20060024700A1

September Information:
APPLICANT: Michele Cargill

APPLICANT: Hongjin Huang

TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519, ORD

CURRENT APPLICATION NUMBER: US/11/124,367A

CURRENT FILING DATE: 2005-05-09

PRIOR FILING DATE: 2004-05-07

PRIOR PLING DATE: 2004-06-07

PRIOR PLING DATE: 2004-06-05

PRIOR PLING DATE: 2004-06-05

PRIOR PLING DATE: 2004-06-05

PRIOR FILING DATE: 2004-06-09

NUMBER OF SEQ ID NOS: 34460

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 433

LENGTH: 2801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LEDCKDIENL-----ESFTDVLDNEGALTS-NWEQWDT-------YCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7; Length 2801;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.2%; Score 140.5; DB 7;
19.9%; Pred. No. 0.56;
tive 89; Mismatches 242;
                                                                                                                                                                                                                                                                               355 EEDEEDEEDVDDEDHDEGF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 19.99
Matches 131; Conservative
                                                                                                                                                                       2204 EEPSRRRPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-11-124-367A-433
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2239
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                                            140 AQLNS--EDSQSVSDSLYYPDSLFSV------KONPLPSSFPGKKITSRAAAPVC 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             397 DDDISDIFSEPGYENDSVEDLK------EVTSISSRKRGKRRYFWEYSEQLTPS 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495 LLQIGNELRKINKVISDLTPVSEL-----PLTARPRSRKEKN---KLAFRACRLKK 542
                                                                                                                                                                                                                                                     -----GSEHELSENEEEEEEEDYEDDK
                                                                       | | :| | ::| | ::| | 2089 RQLRTRKEKARALEDLVDFKE-LFSAPGHTEESMTIDKNTKIPCKSPPPELTDTAT----
                                                                                                                                    187 SSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQ
                                                                                                                                                                                                                          247 QS----RPLLSQIHTDAAKENTCYCGAVAKROEKKGMEPLQGHATPALPFKETQELLLSP
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                                                                                                                                                                                                                                                                                                                                                                                                        EEDEEDVDDEDHDEGF-----
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Search completed: February 28, 2006, 09:02:38 Job time : 19.0827 secs

5.1.7	Biocceleration Ltd.
version	- 2006
GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

; Search time 38.9699 Seconds February 28, 2006, 08:45:35 Run on:

(without alignments)
1577.691 Million cell updates/sec

Title:

US-10-717-665A-44 3349 1 MPQPSVSGMDPPFGDAFRSH.....TAEGNPTGGLVGLRIPTSKV 639 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		*				
Result No.	Score	Query	Length	DB	QI.	Description
				i		
-4	209	6.2	707	Н	DNIMS	nucleolin - mouse
7	202	6.9	712	7	JH0148	nucleolin - rat
m	188	5.6	2761	8	T29285	hypothetical prote
4	184	5.5	1089	~	S48244	_
Ŋ	180.5	5.4	694	Ч	DNCHNL	nucleolin - chicke
9	179	5.3	990	7	T38274	probable transcrip
7	174	5.2	707	7	A35804	nucleolin - human
8	168.5	5.0	1187	7	T46637	transcription fact
σ	166.5	5.0	412	7	A55320	immunophilin FKBP4
10	165.5	6.4	1063	~	A40253	acidic nuclear pro
11	165	4.9	678	~	A54514	glutamic acid-rich
12	165	4.9	1038	~	S52522	hypothetical prote
13	164.5	4.9	1082	~	T50650	
14	164	4.9	916	~	S22864	DNA topoisomerase
15	163.5	4.9	802	٦	S48529	
16	162.5	6.4	713	~	A27441	nucleolin - Chines
17	162.5	4.9	836	7	S49940	cell division cont
18	161	4.8	831	7	S39835	hypothetical prote
19	161	4.8	885	7	G71608	ATP-dept. acyl-CoA
20	160.5	4.8	1877	~	T21861	hypothetical prote
21	160.5	4.8	1974	~	T16703	hypothetical prote
22	160	4.8	500	~	S55785	nucleolar protein
23	160	4.8	1188	7	T46608	zinc finger protei
24	159.5	4.8	1128	~	G86266	hypothetical prote
25	159	4.7	736	~	G01522	•~
26	159	4.7	1085	~	S55352	IFH1 protein - yea
27	159	4.7	1115	7	T41342	17
28	158.5	4.7	1611	~	T38236	Н.
53	158.5	4.7	3488	7	T34418	hypothetical prote

F;395-458/Domain: ribonucleoprotein repeat homology «RRM2» F;397-402/Region: RNA-binding RNP2 motif F;431-438/Region: RNA-binding RNP1 motif F;489-551/Domain: ribonucleoprotein repeat homology «RRM3» F;489-494/Region: RNA-binding RNP2 motif

11:

30 158 4.7 1969 2 T38495 31 155.5 4.7 1151 2 T24541 32 156.5 4.7 1652 2 S38149 34 156 4.7 1695 1 A49795 35 155.5 4.6 1280 2 T010365 36 155.5 4.6 1280 2 T010365 39 155 4.6 140 2 T010365 30 155 4.6 140 2 T010365 30 155 4.6 140 2 T010365 40 154.5 4.6 1190 2 S47536 41 154.5 4.6 1190 2 S47536 42 153 4.6 1190 2 S67701 43 153.5 4.6 1190 2 S67701 44 153 4.6 1190 2 S67701 45 153 4.6 792 2 T42963	hypothetical prote	hypothetical prote	SIS2 protein - yea	myosin-like protei	Alzheimer's diseas	major merozoite su	hypothetical prote	hypothetical prote	Fas-binding protei	erythrocyte-bindin	myelin transcripti	oxysterol-binding	nestin - golden ha	hypothetical prote	hypothetical prote	hypothetical prote
	T38495	T24541	S38149	S38173	A49795	A45948	T00365	T01029	T03847	A37793	T30189	847536	T34518	T38817	S67701	T42963
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	1969	1151	295	1875	695	1726	1280	669	740	1435	1182	1190	1804	992	610	792
30 158 31 157.5 32 156.5 34 156.5 35 156.5 36 155.5 37 155.5 40 154.5 41 154.5 42 154.5 44 154.5 44 154.5	4.7	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6
0 H R R R R R R R R R R R R R R R R R R	158	157.5	157	156.5	156	156	155.5	155	155	155	154.5	154.5	154	153.5	153	153
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C.Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A29958; A40769; A56240; 184688
R;Bourbon, H.M.; Lapeyre, B.; Amalric, F.
J; Mol. Biol. 200, 627-638, 1988
A;Title: Structure of the mouse nucleolin gene. The complete sequence reveals that each F
A;Reference number: A29958; MUID:88316930; PMID:3137346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCTOSS-references: UNIPROT: P09405; UNIPARC: UPI0000009C3; GB:X07699; NID:953453; PIDN:C7 R; Pasternack, M.S.; Bleier, K.J.; McInerney, T.N.
J. Balol. Chem. 266, 14703-14708, 1991
Ashille: Granzyme A binding to target cell proteins. Granzyme A binds to and cleaves nucl A; Reference number: A40769; MUID:91317840; PMID:1860869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A;Residues: 2-20, "X', 22-24 cPAS>
A;Cross-references: UNIPARC:UPI00001739CF
R;Yang, T.H.; Tsai, W.H.; Lee, Y.M.; Lei, H.Y.; Lai, M.Y.; Chen, D.S.; Yeh, N.H.; Lee, S.
Mol. Cell: Biol. 14, 6068-6074, 1994
A;Title: Purification and characterization of nucleolin and its identification as a trans
A;Reference number: A56240, MUID:94344117; PMID:8065340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R,Bourbon, H.
Gene 68, 73-84, 1988
A,Title: Sequence and structure of the nucleolin promoter in rodents: Characterization of A,Reference number: 148118; MUID:89121496; PMID:2906027
A,Reference number: 148118; MUID:89121496; PMID:2006027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI000016CF68; GB:M22089; NID:g200111; PIDN:AAA19841.1; PID:c
C;Comment: This housekeeping protein is involved in the synthesis, packaging, and maturat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 6/3; 45/3; 211/1; 273/1; 302/1; 349/2; 391/1; 432/3; 484/1; 525/2; 566/1; 608/ C; Superfamily: nucleolin; ribonucleoprotein repeat homology C; Reywords: DNA binding; duplication; nucleus; phosphoprotein; RNA binding; transcriptior F; 310-375/Domain: ribonucleoprotein repeat homology <RRM1> F; 311-316/Region: RNA-binding RNP2 motif F; 349-356/Region: RNA-binding RNP2 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 2-19;558-567 <YAN>
A;Cross-references: UNIPARC:UP100001739D0; UNIPARC:UP100001739D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-44 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-707 <BOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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                                                                                          nucleolin - mouse
RESULT 1
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A;Molecule type: protein
A;Residues: 651-703 <LIS>
A;Cross-references: UNIPARC:UP1000017723B
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Best Local Similarity
Matches 107; Conserv
A; Accession: A24088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         363
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cipate: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 23-Jul-1999
CiAccession: JHOA48; A24088; I63130
Giane 88, 187-196, 1990
A;Title: Nucleolin gene organization in rodents: highly conserved sequences within three A;Reference number: JHO148; MUID:90269607; PMID:2347493
A;Accession: JHO448
A;Accession: JHO448
A;Residues: 1-712 <BOU>
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                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 --PTTPFNLFIGNLNPNKSVNELKFAISELFARNDLAVVDVRTGTNRKFGYVDFESAEDL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 LSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIH 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KAVATPAKKNITPAK----- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VIPTPGKKG-----VAQQAKALVPTPGKKGAATPAKGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 TPNPKKLLQI-----GNELRKLNKVISDLTPVSELPLTARPRSRKEKNKLAFRACRLK- 541
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                                                                                                                                                                                                                                                                                                                                                                                 PKEVEEDSEDEEMSEDE----DDSSGEEEVVIPOK-KGKKATTTPAKKVVVSQTKKAAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDAAKENTCYCGAVAKROEKKGMEPLOGHATPALPFKETOELLLSPLP-QEGPGSLAAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSSLSASTSVSDSSQKKEEHNYSLFVSDN-----LGEQPTKCSP----EEDEED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 NRDTLPSNMYQKN-----TDHHGKYAVKK-------SRR-----TDVEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ILIKDTLGLPVAGQTSEFVNQVLEKTA----
                                                                                                                                                                      Query Match 6.2%; Score 209; DB 1; Length 707;
Best Local Similarity 21.0%; Pred. No. 0.0012;
Matches 128; Conservative 78; Mismatches 180; Indels 224; Gaps
                                                                                                                                                                                                                                                                                                                137 PTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSSKTLQAEVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI000017723A
A;Note: the authors translated the initiation codon GTG for 1
R;Lischwe, M.A.; Cook, R.G.; Ahn, Y.S.; Yeoman, L.C.; Busch,
Biochemistry 24, 6025-6028, 1985
                         F;570-634/Domain: ribonucleoprotein repeat homology <RRM4>
F;571-576/Region: RNA-binding RNP2 motif
F;607-614/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EEDVDDEDHDEGFGSEHELSENEEE------
F;524-531/Region: RNA-binding RNP1 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TP--AKKAAVTPGK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257
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A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: NNA
A;Residues: 'NN', 2-44 <RES>
A;Acsidues: 'NN', 2-44 <RES>
C;Coss.references: UNIPARC:UPI0000170A72; GB:M22090; NID:g205793; FIDN:AAA41733.1; PID:C
C;Comment: This protein is the major nucleolar-specific protein in eukaryotic exponential
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Introns: 5/3; 44/3; 211/1; 274/1; 303/1; 350/2; 392/1; 433/2; 485/1; 526/2; 571/1; 613/
C;Superfamily: nucleolin; ribonucleoprotein repeat homology
A;Reference number: 148118; MUID:89121496; PMID:2906027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29285
R;Du, Z.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C34D4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP-----EEDEEDEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTKKAAVPTP--AKKAAVTPG--------KKAAATPAKKAVTPAKVVPTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 DEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ESKKMAPPPKEVEEDSEDEEBSEDE----DDSSGEEEVVIPOK-KGKKATTTPAKKVVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GKKGAAQAKALVPTPGKKGA-----vTPAKGAKN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60; Mismatches 171; Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%; Score 202; DB 2; Length 712; 22.4%; Pred. No. 0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;311-376/Domain: ribonucleoprotein repeat homology «RRM1»
F;399-459/Domain: ribonucleoprotein repeat homology «RRM2»
F;489-552/Domain: ribonucleoprotein repeat homology «RRM3»
F;575-539/Domain: ribonucleoprotein repeat homology «RRM3»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Keywords: DNA binding; nucleus
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NiAlternate names: nucleolar protein C23
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S08414; S10766; A32725; I50397; B30099
R;Maridor, G.; Nigg, E.A.
Nucleic Acids Res. 18, 1286, 1990
A;Title: cDNA sequences of chicken nucleolin/C23 and NO38/B23, two major nucleolar protei
A;Reference number: S08414; MUID:90206792; PMID:2320420
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A;Molecule type: mRNA
A;Residues: 1-694 «MRX»
A;Cross-references: UNIPROT:P15771; UNIPARC:UPI00001308C6; EMBL:X17199; NID:g63710; PIDN:
R;Maridor, G.; Krek, W.; Nigg, E.A.
                                                    R; Varmus, H.E.

#ubmitted to the EMBL Data Library, May 1995

#yReference number: $64738

#yRolecule type: DNA

#yRolidues: 'MYQQ',3-1089 <VAR>
#yRolidues: 'MYQQ',3-1089 <VAR>
C;Genetics: C;Genetics: WIPARC:UPI0000168A23; EMBL:U28158; NID:g967212; PID:g967213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      967 ---ERKAEBEELERQFQKMMQESIDARKSEKVVASKIPVISKPVSVQKPLLLKKSBEPSSS 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 ISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQ-----NPLPSSFPGK-KITSRAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         707 İNNOPNPFYLNYSDP------PDNYFRIQLVTTILLNINRTPAAFTKKCKLLLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 PVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKT-----NMYHNEKVNFHVECKDYVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        755 -FFEYYTFIKEQPL------PKETEFRVSSTFKKYENIFGNTK------FER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 AKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478 KKSRRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVSELPLTAR-----PRSR
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.5%; Score 184; DB 2; Length 1089;
Best Local Similarity 20.2%; Pred. No. 0.04;
Matches 98; Conservative 69; Mismatches 159; Indels 160; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI000013026A; EMBL:U28158
                                                                                                                                                                                                                                                                                  A;Gene: SGD:NMD2; IFS1
A;Cross-references: SGD:S0001119; MIPS:YHR077c
A;Map position: 8R
A,Introns: 2/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 LKRSFD 1089
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     A;Residues: 1-1089 <LEE>
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A;Residues: 'MYQO',3-1089 <FAV>
A;Residues: 'MYQO',3-1089 <FAV>
A;Cross-references: UNIPARC:UPI0000168A23; EMBL:U10556; NID:g500825; PID:g500836; MIPS:X
R;Lee, S.I.; Umen, J.G.; Varmus, H.E.
Proc. Natl. Acad. Sci. U.S.A. 92, 6587-6591, 1995
A;Title: A genetic screen identifies cellular factors involved in retroviral -1 frameshi
A;Reference number: S64648; MUID:95327692; PMID:7604038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P38798; UNIPARC:UPI000013026A; EMBL:U14974; NID:g555938; PID R;Favello, T. Submitted to the EMBL Data Library, June 1994 A;Description: The sequence of S. cerevisiae cosmid 9205. A;Reference number: 846795 A;Accession: 846915.
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2761 < DUZ>
A;Residues: 1-2761 < DUZ>
A;Cross-references: UNIPROT:Q18447; UNIPARC:UP1000007762A; EMBL:U58755; PIDN:AAB00699.1;
A;Experimental source: strain Bristol N2; clone C34D4
                                                                                                                                                                                                            A;Map position: 4
A;Introns: 120/1; 201/3; 365/3; 445/2; 509/1; 728/3; 856/3; 902/3; 940/3; 1027/3; 1508/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.Alternate names: IFSI protein; protein YHR077c
C;Species: Saccharomyces cerevisiae
C;Date: 28-Oct-1994 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C;Accession: S48244; S46815; S64648; S64738
R;He, F.; Jacobson, A.
submitted to the EMBL Data Library, September 1994
A;Description: Identification of a novel component of the nonsense-mediated mRNA decay
A;Reference number: S48244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1882
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                                                                                                                                                                                                                                                                                                                                                                                                    170 SSFPGKKI----TSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 EEDE-------EDEEDVDDED---HDEGFGSEHELSENEEEEEE 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYEDDKDDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERML 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 ----VAKRQEKKG------MEPLQGHATPALPFKETQELLLSPLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEGPGSLAAGESSSLSAS-----TSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP
                                                                                                                                                                                                                                                                                     Ouery Match 5.6%; Score 188; DB 2; Length 2761; Best Local Similarity 22.3%; Pred. No. 0.076; Matches 88; Conservative 56; Mismatches 131; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 NFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMD2 protein - yeast (Saccharomyces cerevisiae)
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Molecule type: DNA
Residues: 1-1089 <HEF>
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A,Gene: CESP:C34D4.14
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Db 329 LSAEDMDKALQLNGKKLMGLEIKLEKAKSKESLKENKKERDARTLFVKNLPYRVTEDEMK 388 Qy 529 EKUKLAFRACRLKKKAQYEANKVKLMGLNTEYDNLLFVINSIKQEIV 575 :	SULT 6 B274 Doable transcription ini Species: Schizoeaccharom Date: 03-Dec-1999 Harris, D.; Squares, R.; Harris, D.; Squares, R.; Harris, D.; Squares, R.; Entred to the EMBL Data Reference number: 221782 Reference number: 221782 Reference number: 121782 Reference: DIA Rosinus: preliminary; tra Molecule type: DNA Residues: 1-990 cHAR> Cross-references: UNIPRC Experimental source: str Ganetics: Ganetics: Ganetics: Keywords: transcription	Query Match 5.3%; Score 179; DB 2; Length 990; Best Local Similarity 21.1%; Pred. No. 0.064; Matches 107; Conservative 72; Mismatches 129; Indels 198; Gaps 23; Qy 238 AKVKINPVQQSRPLLSQIHTDBAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKE 294 Db 26 ASVKINSTRASPNGSDLLND-DSEAAKITTNEKQSSPVDSH 65	QY 295 TQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKC 352 Db	Qy 402 DTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQ 445	Qy 446QERMIRPSEWNRDTLP 461 	Qy 462 SNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKVISDLFP- 514	Qy 515VSELPLTARPRSRKEKNKLAFRACRLKKKAQ- 545 	Qy 546 YEANKVKLWGINTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKD 599 ::: :: ::	Qy 600 TLGLPVAGQTSEFVNQVLEKTAEGNP 625 : :: : : ::
Biochim. Biophys. Acta 1049, 126-133, 1990 A,Title: Structure and developmental expression of chicken nucleolin and NO38: coordinat A,Reference number: \$10766; MUID: 90304215; PMID: 2114180 A,Accession: \$10766 A,Status: nucleic acid sequence not shown A,Molecule type: mRNA A,Residues: 1-694 «MAR2> A,Gross-references: UNIPARC: UPI00001308C6 R,Peter, M: Nakagawa, J.; Doree, M.; Labbe, J.C.; Nigg, E.A. Cell 60, 791-801, 1990 A,Title: Identification of major nucleolar proteins as candidate mitotic substrates of charactering and another a	A; Residues: 56-67;63-109;197-214 <pet> A; Residues: 56-67;63-109;197-214 <pet> A; Residues: 56-67;63-109;197-214 <pet> A; Cross-references: UNIPARC:UPI00001739D2; UNIPARC:UPI00001739D3; UNIPARC:UPI00001739D4 A; Cross-references: UNIPARC:UPI00001739D2; UNIPARC:UPI00001739D3; UNIPARC:UPI00001739D4 A; Fitle: Major Nucleolar Proteins Shuttle between Nucleus and Cytoplasm. A; Reference number: 150397; MUID:89119560; PMID:2914325 A; Accession: 150397 A; Accession: 150397 A; Accession: 150397 A; References: UNIPARC:UPI000000000000000000000000000000000000</pet></pet></pet>	F;37-448/Domain: Thomicleoproclain repeat nomology kRM2> F;373-448/Domain: RNA binding #status predicted <rna2> F;462-525/Domain: RNA binding #status predicted <rna3> F;462-525/Domain: RNA binding #status predicted <rna3> F;463-538/Domain: RNA binding #status predicted <rna3> F;554-618/Domain: RNA binding #status predicted <rna4> F;555-611/Domain: RNA binding #status predicted <rna4> F;655-631/Domain: RNA binding site: phosphate (Thr) (covalent) (by cdc2 kinase) #status predicted</rna4></rna4></rna3></rna3></rna3></rna2>	Query Match 5.4%; Score 180.5; DB 1; Length 694; Best Local Similarity 21.2%; Pred. No. 0.035; Matches 117; Conservative 74; Mismatches 209; Indels 151; Gaps 23; Qy 193 AEVPLSDCVQRASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINBVQQSRP 250	QY 251 LLSQIHTDAAKENTCYCGAVAKRQBKKGMEPLQGHATPALPFKETQELLLSPLPQ 305 DD 54 AVTPAKKAATPAKKAATPAKKAVFPAKKAVATPAKKAVAPSFK 96	QY 306 EGPGSLAAGESSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP 354 i	QY 355	QY 375 SEHELSENEEEEEEEDYEDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRR 432	QY 433YFWEYSEQLTPSQQERMIRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRR 482 Db 276 TPASAFSLFVKNLTPTKDYEEIRTAIKEFFGKKNLQVSEVRIGSSKRFGYUP 328	OY 483 TDVEDLTPNPKKLLOIGNELRKLNKVISDLTPVSELPLTARPRSRK 528

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transcription factor 1, neural - rat

NyAlternate names: neural zinc finger factor-1

C;Species: Rattus norvegicus (Norway rat)

C;Accession: T46637

R;Jiang, Y.; Yu, V.C.; Buchholz, F.; O'Connell, S.; Rhodes, S.J.; Candeloro, C.; Xia, Y.F.
J. Bhol. Chem. 271, 10723-10730, 1996
A;Title: A novel family of Cye-Cye, His-Cye zinc finger transcription factors expressed i
A;Reference number: A58210; MUID:96210003; PMID:8631881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: binds specifically to a cis-regulatory element of the beta-retinoic acid e nervous system and in the pituitary gland C;Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:P70475; UNIPARC:UP100000E86A7; EMBL:U48809; NID:91511631;
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                                                                                                                                                                                                                                                                                                                                                                                                     494
                                                                                                                                                                                                                                                                                                                              252 DDEDDDDEDDEEEEEEEEEPVKEAPGKRKKEMA----KQKAAPEAKKQKVEGTEPTTA 306
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                                                            191
                                                                                                                               398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 ALELTGLKVFGNEI-KLEK-------PKGKDSKKERDARTL-LAKNLPYKV 404
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                                      -----LSENEEEEEEEDYEDDKDD
                                                                                                                                                                  -----WNRD-----TLPSNMYQKNGLHHGKYAVKKSRR-----TDVEDLTPNPKK
--TKCSPEEDEED
                                                                                                                                                                                                                                                                  DISDIFSEPGYENDSVEDLKEVISISSRKRGKRRYFWEYSEQLIPSQQERMLRPSE----
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309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQP-
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Pred. No. 0.28;
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                                                                                                                                      EEDVDDEDHDEGFGSEHE----
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Best Local Similarity 27.1%,
Matches 73; Conservative
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A; Residues: 1-1187 <JIA>
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A; Residues: 1-707 < SR2>
A; Cross references: UNIPARC: UPI0000161B7E
A; Cross references: UNIPARC: UPI0000161B7E
B; Ishikawa, F.; Matunis, M.J.; Dreyfuss, G.; Cech, T.R.
A; Ishikawa, F.; Matunis, M.J.; Dreyfuss, G.; Cech, T.R.
Mol. Cell. Biol. 13, 4301-4310, 1993
A; Rittle: Nuclear proteins that bind the pre-mRNA 3' splice site sequence r(UUAG/G) and the pre-mRNA 3' splice site sequence r(UUAG/G) and the pre-mRNA 3' splice site sequence r(UUAG/G) and the pre-mRNA 3' splice site sequence r(UUAG/G) and the pre-mRNA 3' References: UNIPARC: UPI0000073927
A; Residues: 458-474 < ISH3
A; Residues: 458-474 < ISH3
A; Residues: 458-474 < ISH3
A; Reperimental source: Hela cell nuclei
A; Note: sequence extracted from NCBI backbone (NCBIP:134645)
B; Note: sequence extracted from NCBI backbone (NCBIP:134645)
B; Note: sequence extracted from NCBI backbone (NCBIP:134645)
B; Note: sequence extracted from NCBI backbone (NCBIP:134645)
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B; Note: sequence extracted from NCBIP:134645)
B; Note: sequence 
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A; Residues: 1-707 <SRI>
A; Residues: 1-707 <SRI>
A; Residues: 1-707 <SRI>
A; Cross-references: UNIPROT: P19338; UNIPARC: UPI000161B7E; GB: M60858; GB: J05584; NID: g18
R; Srivastava, M.; Fleming, P.J.; Pollard, H.B.; Burns, A.L.
FEBS Lett. 250, 99-105, 1989
A; Title: Cloning and sequencing of the human nucleolin cDNA.
A; Reference number: S04631; MUID: 89290043; PMID: 2737305
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A;Rebidues: 231-236;349-362;399-403;458-461;655-656,'X',658-660 <JOR>
A;Cross-references: UNIPARC:UPIO00017723C; UNIPARC:UPI000017723D; UNIPARC:UPI000017723B;
A;Experimental source: surface-labelled HeLa cells
                                                                                                                                                                                               NiAlternate names: phosphoprotein pp100; protein B50; protein C23
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 09-Jul-2004
C;Accession: A35804; S04631; Ä48138; A55996
R;Srivastava, M.; McBride, O.W.; Fleming, P.J.; Pollard, H.B.; Burns, A.L.
A;Title: Genomic organization and chromosomal localization of the human nucleolin gene.
A;Reference number: A35804; MUID:90368666; PMID:2394707
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5.2%; Score 174; DB 2; Length 707;
Best Local Similarity 20.4%; Pred. No. 0.078;
Matches 99; Conservative 76; Mismatches 162; Indels 148; Gaps
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Superfamily: nucleolin; ribonucleoprotein repeat homology

;Reywords: DNA binding; nucleus; nucleus; phosphoprotein;

;308-373/Domain: ribonucleoprotein repeat homology «RRM1>

;394-456/Domain: ribonucleoprotein repeat homology «RRM2>

;487-550/Domain: ribonucleoprotein repeat homology «RRM3>

;573-634/Domain: ribonucleoprotein repeat homology «RRM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: not compared with conceptual translation A;Molecule type: mRNA
          451
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;Cross-references: GDB:125908; OMIM:164035
       ---IRISSLITEGVNPTLDEVSKFNP
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                                                                                                                                                                             nucleolin - human
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A;Cross-references: UNIPARC:UD1000053123; EMBL:Z49810; NID:g854472; PIDN:CAA89942.1; PII
A;Experimental source: strain AB972
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NyAlternate names: GARP
NyAlternate names: GARP
Species: Plasmodium falciparum
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54514
R;Triggla, T.; Stahl, H.D.; Crewther, P.E.; Silva, A.; Anders, R.F.; Kemp, D.J.
MOI Biochem. Parasitol. 31, 199-202, 1988
A;Title: Structure of a Plasmodium falciparum gene that encodes a glutamic acid-rich prot
A;Reference number: A54514; MUID:89040048; PMID:2903445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Cross-references: UNIPROT: P13816; UNIPARC: UP1000012B0E0; GB: J03998; NID: g160298; PIDN: A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 TQELLLSPLPQEGPGSLAAGESSSLS-----ASTSVSDSSQ-----KKEEHNYSLFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 EKEAKSEPQQPEDNAETAATEQVSSSNGPATDDAQATLNTDSSEANEIVKKEEG-----
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4.9%; Score 165; DB 2; Length 67
Best Local Similarity 22.3%; Pred. No. 0.22;
Matches 61; Conservative 44; Mismatches 101; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.9%; Score 165.5; DB 2;
Best Local Similarity 23.2%; Pred. No. 0.36;
Matches 90; Conservative 50; Mismatches 109;
                                                                                                                                                                                       A,Cross-references: SGD:S0004470; MIPS:YML010w
A,Map position: 131
C,Keywords: nucleus; tandem repeat
F;148-216,Region: aspartic acid/glutamic acid-rich
F;931-1063/Region: 6-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 497 QIGNELRKLNKVISDLTPVSELPLTARP 524
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C;Superfamily: histone H1
C;Keywords: tandem repeat
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A;Status: preliminary
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356 YISQKL
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                                                                                                                                                A;Gene: SGD:SPT5
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                                                                                                         C, Genetics
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C; Date: 06-Feb-1995 #seq
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C;Superfamily: yeast peptidylprolyl isomerase FPR3; BKBP-type peptidylprolyl isomerase h
C;Keywords: nucleus; phosphoprotein
F;324-371/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
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A; Residues: 1-1063 <SWA>
A; Residues: 1-1063 <SWA>
A; Residues: 1-1063 <SWA>
A; Cross-references: UNIPROT: P27692; UNIPARC: UPI0000053123; GB: M62882; NID: g172679; PIDN: R; Genter to the EMBL Data Library, June 1995
A; Reference number: S55102
A; Accession: S55109
A; Accession: S55109
A; Residues: 1-1063 <GEN>
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NyAlternate names: protein YM9571.08; protein YML010w
C;Specias: Saccharomyces cerevisiae
C;Specias: Saccharomyces cerevisiae
C;Accession: A40253; S55109
R;Swanson, M.S.; Malone, E.A.; Winston, F.
Mol. Cell. Biol. 11, 3009-3019, 1991
A;Tile: SPTS, an essential gene important for normal transcription in Saccharomyces A;Reference number: A40253; MUD:91246167; PMID:1840633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
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                                                                                                                                                Species: Spodoptera frugiperda (fall armyworm)
Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 QEKKGMEPLQGHATPALPFKETQEL-----LLSPLPQEGPGSLAAGESSSLSAST
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Db 511 LIGTIGRVNVVPRRDNHKKKMAKIEEAELQKQKHVDKEEDKKEESKE 557 Qy 279 MEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYS 338	Db 910 KEKARVNYDKHKSELKPSLDKGDVVDDIIPVFAPWPALLKYKYKVKIQPGSAKKT- 964 Qy 545 QYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEI 595 Db 965
Qy 399 DISDTFSEPGYENDSVEDLKEVTSISSRKRGKRR 432 	man
RESULT 12 S5252 hypochetical protein YPL009c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein LPA8c; hypothetical protein YP8132.04c C;Species: Saccharomyces cerevisiae C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004 C;Accession: S52522; S59684 R;Badcock, K.; Churcher, C. Badcock, K.; Churcher, C. B. Reference number: S62519	C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004 C;Accesaton: T50650 C;Accesaton: T50650 A;Tile: Beta-NAP, a cerebellar degeneration antigen, is a neuron-specific vesicle coat I A;Reference number: 225157; MUID:95401267; PMID:7671305 A;Accesaion: T50650 A;Accesaion: T50650 A;Accesaion: T50650 A;Accesaion: T50850 A;Accesaion: T50850 A;Accesaion: T50850 A;Accesaion: T50850 A;Accesaion: T50850 A;Accesaion: T50850 A;Accesaion: T50850 A;Accesaion: T50850 A;Accesaion: T50850 A;Accesaion: T50850 A;Cross-references: UNIPROT:013367; UNIPARC:UPI0000125030; EMBL:AF022152; PIDN:AAB71894.]
PI0000052E40; EMBL:Z48483; NID:G683777; PIL	Query Match 4.9%; Score 164.5; DB 2; Length 1082; Best Local Similarity 22.1%; Pred. No. 0.41; Matches 90; Conservative 59; Mismatches 150; Indels 109; Gaps 17;
A; Experimental gource: strain AB972 R; Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; Wa submitted to the EMBL Data Library, August 1995 A; Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.	Qy 176 KITSRAAAPUCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNF 227
A;Reference number: S59677 A;Accession: S59687 A;Accession: S59684 A;Molecule type: DNA A;Residues: 1-1038 HTTP://document.org/	OY 228 HVECKDYVKKAKVKINPVQOSRPLLSQIHTDAAKBNTCYCGA 269 : : :
A;Cross-references: UNLPAKC:UF10000052E40; EMBL:U55555; NID:9765076; FID:9765004; MIES-1 C;Genetics: A;Cross-references: SGD:S0005930 A;Map position: 16L	OY 270 VAKROBKKGMEPLOGHATPALPFKETOELLLSPLPQEGPGS 310 ::
Query Match 4.9%; Score 165; DB 2; Length 1038; Best Local Similarity 20.8%; Pred. No. 0.37; Matches 103; Conservative 73; Mismatches 175; Indels 144; Gaps 21;	QY 311 LAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDVDDEDHD 370 : : :
Qy 201 VQKASKPPSSTQIMVKTIMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLS 253	Qy 371 E-GFGSEHELSENEEEEEEEDYEDDXDDDISDTFSEPGYENDSVEDLKEVT 421
Qy 254 QIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGS 310	Qy 422 SISSRKRGKRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNWYQKNGLHHGKYAVKKSR 481
OY 311 LAAGESSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEBDVDDEDHD 370	QY 482 RIDVEDLIPNPKKILQIGNELRKINKVISDLIPVS 516
Qy 371 EGFGSEHELSENEEEBEEEDYEDDXDDDISDTFSEPGYENDSVE-DLKE 419	RESULT 14 S22864 DAYA FORGETS SEE GO 1 2) T - Arabidonsis Phalians
QY 420	C.Species Arabidopsis thaliana (mouse-ear cress) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004 C;Accession: S22864
QY 439 EQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTP 490	R;Kteber, J.K.; Signer, E.K. submitted to the EMBL Data Library, September 1990 A;Description: Cloning and characterization of an Arabidopsis TOP1 gene. A;Reference number: S22864
491	A,Accesion: S22864 A,Molecule type: mRNA A,Residues: 1-916 <kie></kie>

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A;Experimental source: strain S288C (AB972)
R;Sugimoto, K.; Matsumoto, K.; Kornberg, R.D.; Reed, S.I.; Wittenberg, C.
Mol. Gen. Genet. 248, 712-718, 1995
A;Title: Dosage suppressors of the dominant Gl cyclin mutant CLN3-2: identification of A;Reference number: S60122; MUID:96069710; PMID:7476874
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  A;Cross-references: UNIPROT:P30181; UNIPARC:UP1000013712B; EMBL:X57544; NID:g16557; PID:
C;Genetics:
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                                                                                                                                                                                                                                                                                                                     61 VTSPNGTIPSNKTSIVKSSMPSSSSKASPAKSPLRNDMPSTVKDRSQLQ------ 109
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                                                                                                                                                                                                                                                                                                                                                                                              161 -RASRIIKDESDDETPISSMFRKKIDSGMSGGNQLSNDEKKPLVQKLHQNGSTVKNEVPN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 GKV-----LGKRPLEKNSSADQSSLKKAKISASPTSVKMKQDSVKKEIDDKGRVLVSPKM 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENEREBEBEBEDYEDDKDDD--ISDTF-SEPGYENDSVEDLKEV--TSISSRKRGKRRYFW 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLTPVSELPLTARPRSRK--EKNKLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVIN 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494
                                                                                                                                                                                                             111 GTKEVDYLGLDDFSSPYQDEEVIS--KTPTLAQLNSEDSQSVSD-SLYYPDSLFSVKQNP 167
                                                                                                                                                                                                                                                                                        168 LPS---SFPGKKIT-SRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EYSEQLTPSQQERMLRPSEWNRD------TLPSN-----MYQKNG---LH 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : :: : | | : : | : : | : : | 335 SPRSRAMTKNTKUTKUSKYSTSSKSSPSSGDGQKKWTTLVHNGVIFPPPYKPHGIKILY 394
                                                                                                                                                                                                                                                2 GTETVSKPVMDNGSGDSDDDKPLAFKRNNTVAS-NSNQSKSNSQRSKAVPTTKVSPMRSP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 GHATPALPFKETQELLLSPL-----PQEGPGSLAAGESSSLSASTSVSDSSQKKEEHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 KAKOLSTREDGTDDDDDDDDVPİSKRFKSDSSNSNTSSAKPKAVKLNSTSSAAKPKARNVV
                                                                                                                                                                      Gaps
                                                                                                                              Query Match
4.9%; Score 164; DB 2; Length 916;
Best Local Similarity 21.1%; Pred. No. 0.35;
Matches 124; Conservative 98; Mismatches 226; Indels 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: eukaryotic type I DNA topoisomerase
C;Keywords: DNA binding; DNA replication; isomerase
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                                                  A; Gene: TOP1
C; Superfamily:
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NAB3 protein - yeast (Saccharomyces cerevisiae)
NyAlternate names: probable RNA/ssDNA-binding protein HWD1; protein P1945; protein YPL19
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S48229; S65209; S60122
R;Wilson, S.M.; Oberdorf, A.M.; Datar, K.V.; Swedlow, J.R.; Paddy, M.R.; Swanson, M.S.
Submitted to the EMBL Data Library, January 1994
A;Description: Characterization of Nuclear Polyadenylated RNA-Binding Proteins from Sacch A;Accession: S48529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Reaidues: 1-802 <WIL>
A;Reaidues: 1-802 <WIL>
A;Reaidues: UNIPROT:P38996; UNIPARC:UPI000004F979; EMBL:U05314; NID:g476219; PID
A;Cross-references: UNIPROT:P38996; UNIPARC:UPI000004F979; EMBL:U05314; NID:g476219; PID
B;Rieggar, M.; Mueller-Auer, S.; Schaefer, M.
B;Reference number: S65202
A;Reference number: S65209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Residues: 1-802 <RIE>
Cross-references: UNIPARC:UP1000004F979; EMBL:Z73546; NID:g1370396; PID:g1370397; GSPD
RESULT 15
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A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-340,'1',342-802 <SUG>
A;Cosa-references: UNIPARC:UPI0000694F8; GB:D37935; NID:g1235749; PID:g1235750
C;Genetics:
A;Genetics: A;Genetics: A;Genes: SGD:NAB3; HMD1; MIPS:YPL190c
A;Cross-references: SGD:S0006111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 KKEEHNYSLFVSDNLGEQPTKCSPEEDEE-----DEEDVDDEDHDEGFGSEHELSENEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 TPNPKKLLQIGNEL------RKLNKVISDLTPVSELPLTARP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           429 GKRRYFWEYSEQLIPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          525 ----RSRKEK-----NKLAFRACRLKK---KAQYEANKVKLWGLN-TEYDNL----
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                      A;Map position: 16L
C;Superfamily: yeast NAB3 protein; ribonucleoprotein repeat homology
C;Keywords: nucleus; RNA binding
F;331-396/Domain: ribonucleoprotein repeat homology <RRM1>
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                                                                                                                                                                                                                                                                                                                                      Query Match 4.9%; Score 163.5; DB 1; Length Best Local Similarity 22.1%; Pred. No. 0.32; Matches 76; Conservative 57; Mismatches 112; Indels
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Q9DUNO_HHV8	Q813T6_PLAF7 O8F2J8_LEPIN	090R71 HHV8 07RKZ2 PLAYO	YT521 HUMAN	OBIKH9 PLAF7	Q18447 CAEEL Q7RTH1_PLAYO	O40947 HHV8 O54NP8 DICDI	1 1	
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MEDLINE=99279253; PubMed=10349636; DOI=10.101
Carninoi P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Li F., Yao K.T.;
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EMBL; AN139008; AN28956.1; -; mRNA.
InterPro; IRR04627; TF bzIP.
PROSITE; PS00036; BZIP BASIC; UNKNOWN 1.
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                                                                                                         EEDVDDEDHDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEV
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Mus musculus adult male testis cDNA, RIEN full-length enriched
library, clone:4932441F15 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J; TISSUB=Testis; MEDLINE=210855500; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; Rawai J., Shinaqawa A., Shibata K., Yoshino M., Itch M., Ishii Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
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TATALIA-ESTBL/61, TISSUE=Testis;

The FANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

Than Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

Nature 420:563-573 (2002).
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Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kahl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Asakai K., Okido T., Frunno M., Aono H., Baldarelli R., Barsh G., Barke J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Austinoich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N. H., Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storck K.-F., Whinming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S., Lasachi Y., Vanachi Y., Kawaji H., Kohteuki S.,
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STRAIN=C57BL/6J; IISSUG=Testis;

WEDLINE=2053013; PubMed=1107681; DOI=10.1101/gr.152600;

WEDLINE=2053013; PubMed=1107681; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Akiawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Ishil Y., Nakamura S., Hazama M., Nishine T., Harda A., Amamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Ayoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramateu M., Inoue K., Kira A., Hayashizaki Y., RIKEN integrated sequence R., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format

R RIKEN integrated sequence analysis (RISA) system-384-format

St. Genome Res. 10:1757-1771(2000).
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STRAIN=CSPEL/G1, TISSUE-TESTIS;
OIL 101/GT.145100.
CARNINE=CSPEL/G1, TISSUE-TESTIS;
DOI=10.1101/GT.145100.
CARNINCI P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000)
                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Pred. No. 1.4e-139;
19; Mismatches 22;
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PROSITE; PS00036; BZIP_BASIC; UNKNOWN_1.
Hypothetical protein.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                              121 DDFSSPYQDEEVISKTPTLAQLNSBDSQSVSDSLYYPDSLFSVKQNPLPPSSFPSKKITN
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                                                               1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPFDNFL
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MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
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THE German CDNA CONSORTIUM;
KOEhrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
Koehrer K., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX647573; CAI46104.1; -; mRNA.
INTERPRO; IPRO4827; TF bZIP.
PROSITE; PS00036; BZIP_BASIC; UNKNOWN_1.
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10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp313F2319 (Fragment).
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Q5HYG4;
10-MAY-2005 (TEMBLrel. 30, Created)
10-MAY-2005 (TEMBLrel. 30, Last aguence update)
10-MAY-2005 (TEMBLrel. 30, Last annotation update)
10-MAY-2005 (TEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp686G2059 (Fragment).
Name-DKFZp686G2059;
Homo sapiens (Human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae;
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          Score 3129; DB 2;
Pred. No. 2.9e-139;
2; Mismatches 2;
            93.4%;
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The German cDNA Consortium;
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NCBI_TaxID=9606;
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QBCRR3;
QBCRR3;
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
Hymochetical protein.
Hymochetical fulman).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa; Chordata, Primates; Catarrhini; Hominidae;
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Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A174896; A0018732.1; -; mRNA.
Hypothetical protein.
SEQUENCE 417 AA; 46579 MW; 9DBD37B07C14556B CRC64;
408 AA; 45625 MW; E3E36BFEA8B4284B CRC64;
                                                     64.1%; Score 2148; DB 2; 99.8%; Pred. No. 2.4e-93; tive 0; Mismatches 1;
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Best Local Similarity 99.8
Matches 407; Conservative
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Matches 407; Conservative
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NELINE-257BL/64; TISSUB-Retina;

MEDLINE-257BL/64; TISSUB-Retina;

MEDLINE-257BL/64; TISSUB-Retina;

MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;

MA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S., Aarawa T., Jana A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Matsuda H.A., Ashburner M., Batalov S., Gasavant T., Relschmann W., Gasaterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Putuno M., Aono H., Baldarelli R., Barah G., Bakai K., Okido T., Pletcher C., Fullia M., Mandon P., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whittaker C., Willming L., Willer M., Weltz C., Whittaker C., Wilming L., Willer M., Weltz C., Whittaker C., Wilming L., Willer M., Mandon M., Kawaji H., Kohtsuki S., Kawaji H., Kohtsuki S.,
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STRARLE-GSYBL/GJ; IISSUE-Retina;
STRARLE-GSYBL/GJ; IISSUE-Retina;
The PANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                  AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
                                                       KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
                                                                        Mus musculus (Mouse).
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930040G19 product:hypothetical protein, full insert sequence.
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Q8C8N7;
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RA Adachi J. Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Rabadchi J., Alzawa K., Akimura T., Hara A., Hashizume W., Alzawa K., Hayashida S., Furuno M., Hanagaki T., Haraoka T., Hirozane T., Rayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Ratoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Ratoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Arithara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Raya S., Mishi K., Nomura K., Numazaki R., Ohno M., Ohasto N., Okazaki Y., A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., A Saaki D., Shibata K., Shinagawa A., Shirataki T., Sakai C., Sakai K., Sakazume N., Sano H., A Tagama A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

REMBL, AKO44760; BAC320701; -; mRNA.

RENBL, MGS18MGSG0000000048249; Mus musculus.

MG1, MG11924378; AS30001N09Rik.
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                                                                                                                                                                                                                                                                                                                              STRAIN=CSTBL/6J; TISSUB=Retina; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Itoh M., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matamuro H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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NUCLEOTIDE SEQUENCE.
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RESULT 9
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REDINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

REDINE=21085660; PubMed=11217851; DOI=10.1038/3505500;

A Arakawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

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Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sakai H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Nyasahirat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/67; TISSUE=Retina;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                  Mus musculus (Wouse).
Eukaryota; Watazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last amnotation update)
Mus musculus adult retina cDNA, RIKEN RIKINI-langth enriched library,
clone:A930001N09 product:hypothetical protein, full insert sequence.
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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                           27 MOUSE
Q9CTQ7_MOUSE PRELIMINARY;
Q9CTQ7;
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                                                                                                                                                                                                                                                                      Name=A930001N09Rik;
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     RESULT 8
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
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Hanagaki T., Hara A., Hayatau N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konuo H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C.,
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Sogabe Y., Suzuki H., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatcu M., Hayashizaki Y.,
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO20796; BAB32214.1; -; mRNA.

ENBEL; AKO20796; BAB32214.1; -; mRNA.

M. Hypothetical protein.

M. Hypothetical protein.
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Herradontoidea; Tetraodontidae; Tetraodon.

NCBI_TaxID=99883;
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   S., Kawai
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Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kaw
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.9%; Score 1602.5; DB 2; Length 92.7%; Pred. No. 8e-68; cive 8; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 AA; 36692 MW; 1397555C4934A64B CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAF15001, whole genome shotgun sequence.
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13-SEP-2005 (TrEMBLrel. 31, Last seq
13-SEP-2005 (TrEMBLrel. 31, Last ann
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Q4RRX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 306; Conservative
                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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Score 656; DB 2; Length 131;
Pred. No. 8.5e-24;
6; Mismatches 7; Indels
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09VC61, 08T9A9;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2003 (TrEMBLrel. 23, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
CG13624-PA, isoform A (Cg13624-pb, isoform b) (SD09792p)
ORFNames=CG13624;
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Last annotation update)
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QSZMDS;
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STRAIN=CB; TISSUE=Bursa;
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25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
ORFNames=RCJMB04 2h14
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             Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Adaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
Andaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Antouard V., Jaffer S., Lutfalla G., Dossat C., Segurens B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
A cruaud C., Duprat S., Brottier F., Coutanceau J.P., Gouzy J.,
A rara G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
A kalis M., Volff JM., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Mincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
I. Nature 431:946-957(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 ASCDIWGTKEVDFLGLDDFSSPYQDEEVIGRTPTLAQLNSEDSLPVCEALYPPADL--- 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 NTCYCGAVAKROEKKGMEPLOGHATPALP-FKETOELLLSPLPOEGPGSLAAGESSSLSA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSE 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 NEEEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEVTS-ISSRKRGKRRYFWEYSEQ 440
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NUCLEOTIDE SEQUENCE.

GENOSCOPE: Whitehead Institute Centre for Genome Research;

Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
41.1%; Score 1377.5; DB 2; Length 600;
Best Local Similarity 43.8%; Pred. No. 5.9e-57;
Matches 316; Conservative 74; Mismatches 126; Indels 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     600 AA; 66291 MW; B2F28B2F3B27B1C4 CRC64;
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                               540 RKVNDVNVDLKYILKHFSLSPQVAPPVAGQTSDFVNKILDNTGRGDPTGGLVGLKVPTSK 599
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----LPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSK
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Caldwell R.B., Klerzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
"Full-length cDNAs from chicken bursal lymphocytes to facilitate
genefunction analysis.";
Geneme Biol. 6:R6-R6 (2005).
EMBL; AJ71949; CAG31108.1; -; mRNA.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Amanartidae N. Callers S.E., S.L. P. W. Honkins R. A. Galle R.F.,
St. Genere R.A. Icadis S.E., St.Land S. W. Honkins R. A. Galle R.F.,
Sutton G.G. Worthan J. S., Yandards S. A. Sabhurner W. Henderson S.M.,
Statuton G.G. Worthan J. S., Yandards S. A. Sabhurner W. Henderson S.M.,
Statuton G.G. Worthan J. S., Yandards S. A. Sabhurner W. Henderson S.M.,
Statuton G.G. Worthan J. S., Yandards S. A. Sabhurner W. Henderson G. S.M.,
Sabler R. W. L. Worthan J. S., Yandards S. A. Sabhurner W. Henderson G. S.,
Ballow R. W. Boan P. Bazer E.G., Helt G., Nelson C.R. Millos G.L.G.,
Ballow R. W. Bana P. Sabendan B. S. Banck S. B. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhura I. Sabhur
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622 SKLEDPHVLNEVTDPVFSPTCSVRGIKVYKHSG------KARKGDGNDLTPNARKLH 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 QEGPGSLAAGESSSLSASTSVSDSSQXKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEDV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 DIYCEDLIKYIKLISCDIWGIKEVDYL-----GLDDFSSP-----YQDEEV-- 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IEDFLPQTAV----TQSVNFLLSPQAQGQDALVAPPMELLQQQQQNHQQLQVGS 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 SSNGIGSGSGGYFTPDMSHSLSLANVVSEQVLLOEATTPN-----ELLYEMTPNSNAMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | | | | : | | | | : | | | 357 LPQLQTLLTLSQQQQSNSSSTSPYEIYHSTPQKPQQQQLSASFSFGSQASQSPLTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 DDEDHDEGFGSEH------ELSENEE------EESEEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   562 SSENSDNYDDCSSDNGLSEDEDETRISTPNHLSSSKGKERFFWQXNVQAKGFKGKRLVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 ----RPSEWNRDTLP-----SNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 KTLQAEVPLSDCVQKASKPPSST----QIMVKTNMYHNEKVNFHVECKDYVKKAKVKINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 VQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 SSGFGSSASGNSTTTSNQTS---GSAVRKSFGYQSAVENSQLSRLSSSAPTH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393 EDDKODDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERML--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 -----SPIDVLDNEGALISNWEQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 SDISSAIIHTKHEPFSLDDDYIFPNDKAEIQAADLSDLNGGDFLDVIGN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 SVSGMDPPFGDAF---RSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL-
                                                                                                                                                                                                                                                  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liso G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

-!- INTERACTION:

Q9VL14:CG18619; NbExp=1; IntAct=EBI-150517, EBI-165049;
EMBL; AR003748; AAF56314.2; -; Genomic_DNA.
          Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith
Yu C., Rubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.5%; Score 417; DB 2; Length 755;
                                                                                                                                                                                              Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                           "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IntAct, Q9VC61; -.
Ensembl; CG13624; Drosophila melanogaster.
Flyaase; FBgn0039209; CG13624.
InterPro; IPR004827, TF bZIP.
PROSITE; PS00036; BZIP BASIC; UNKNOWN 1.
SEQUENCE 755 AA; 82263 MW; D851D42235FF10E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::| :||
445 PERS--ILS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.1e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.1%;
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Matches 160; Conservative
                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 MYQKN----GLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVSELP 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 TKCSPREDEEDEBDVDDEDHDEGFGSEHELSENEEEEEEEEDYEDDKDDDISDTFSEPGY 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 ENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQERML-----RPSEWNRDTLPSN 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85
                      LAAGTTSAAVSVGSNAGTSGTAMSRLSSSAPTHISGFEQIWQRREPRPHLLSTGSLAEAG
          QIGNELRKLNKVISDLTPVSELPLTARPRSRKEKNKLAFRACRLKKKAQYEANKVKLWGL
                                                                                                                                                                                               Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Culicidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62; Gaps
                                                                                                                                                                                                                                                                                                                                            The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBI/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.5%; Score 386; DB 2; Length 293; 36.3%; Pred. No. 1e-10; ative 38; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                           "Anopheles gambiae re-annotation.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 293
293 AA; 31535 MW; 0700521A3C593F97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520 LTARPRSRKEKNKLAFRACRLKKKAQYEANKVKLWGLNTEY 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGPO0000015170 (Fragment).
ORFNAMES=ENSANGG0000012681;
                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AAAB01008844; EAA06118.2; -; Genomic_DNA
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                               Anopheles gambiae Sequence Committee;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00036; BZIP BASIC; UNKNOWN 1
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004827; TF_bZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 36.3*
Matches 102; Conservative
                                                                                                                         Q7QG21_ANOGA PRELIMINARY;
                                                                                                                                                                                                                               Anophelinae; Anopheles
                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                       NCBI_TaxID=180454;
                                                    557 NTEY 560
                                                                        EIEH 736
                                                                                                                                                                                                                                                                                                                                    STRAIN-PEST;
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NON TER
SEQUENCE
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327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 YN-----AGLKUEKIENIR----KIGNKSKGKNTILKKIGVHWENKKEMQNEESY- 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287 TPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDIWGTKEVDYLGLDDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQN 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 PLPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVN 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAFRSHTFSE----QTLMSTDLLANSSDPDFMY------ELDREM-----N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 FHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 EQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEEEE-EEEEDYEDDKDDDISDTFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 EPGYENDSVEDLKEVTSISSRKR----GKRRYFWEYSEQLTPSQQERMLRPSEWNRDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-22255706; PubMed=12368865; DOI=10.1038/nature01099; Carlton J.M., Angiuoli S.V., Suh B.B., Koojj T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Perterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 6.8%; Score 227; DB 2; Length 2649; Similarity 19.0%; Pred. No. 0.037; 31; Conservative 110; Mismatches 188; Indels 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                  Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preliminary data.

EMBL; AABL01002172; EAA18637.1; -; Genomic_DNA.
InterPro; IPR011591; Botulinum.
InterPro; P0001963; Botulinum; 2.
Hypothetical protein.
SEQUENCE 2649 AA; 309910 MW; E7207F344643AC24 CRC64;
                                                                                                  Last sequence update)
Last annotation update)
            Z
                                                                      Created)
                                                                  01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, Hypothetical protein.
QTRAS7_PLAYO PRELIMINARY;
Q7RAS7;
                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                        NCBI_TaxID=73239;
                                                                                                                                                                                               Name=PY06422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 131;
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	460 KYKUSKSIIIEYTDSHIREKWKEEKKKQR 485 VEDLTPNPKKLLQIGNELRKLNKVISDLT : : : : : :	QBCE30 MOUSE PRELIMINARY; PRT; 707 AA. QBCE30; QBCE30; O1-MAR-2003 (TrEMBLrel. 23, Created) O1-MAR-2003 (TrEMBLrel. 23, Last sequence update) O1-MAR-2003 (TrEMBLrel. 26, Last annotation update) O1-MAR-2004 (TrEMBLrel. 26, Last annotation update) Mus musculus 10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732495B18 product:nucleolin, full insert sequence. Name=Ncl; Name=Ncl; Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mummalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	(1) NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NUCLEOTIDE SEQUENCE. NEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; NEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; NUCLEOTIDE=109560; PubMed=11277851; DOI=10.1038/35055500;	A Kawan U., Shinadawa A., Shibata K., Tobinion W., 1100 M., 1101 M., 1201 M., Arawa T., Baradawa A., Shibata K., Kiyosawa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Kiyosawa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Gojobori T., Bono H., Ksaukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Fleischmann W., Gasterland T., Mikaido I., Peeolo G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann W., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N., A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., A Hayashizaki Y.;
8 6 8 6 8 6 8	DP OA SOA DP OA OA OA OA OA OA OA OA OA OA OA OA OA	0	RN RR RR RR RR RR RR	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
PSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKVI 509	SUL		parasite Plasmodium yoelii yoelii."; Nature 419:512-519(2002)!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which preliminary data. EMBL; AABLO1001988; BAA18150.1; -; Genomic DNA. SEQUENCE 761 AA; 90874 MW; CEEF787A6E85D5B3 CRC64; SQUENCE 761 AA; 90.34; Pred. No. 0.046; Ouery Match Best Local Similarity 19:34; Pred. No. 0.046; Matches 127; Conservative 106; Mismatches 239; Indels 186	ANSSDPDFMYELDREM : : : SESEDIELEEENDSDII VLDNEGALTSNWEG : : DFDDENEGEDLSDDDF DEEVISKTPTLAGLAS; : : : EENNDERKEUTSIANKEUTING KTLQAEVPLSDCVQKA

488

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---AAQAKALVPTPGKKGAATSAKGA 134
                                                                                                                                                                                                               ----- SEEEEDYEDDK 396
                                                                                                                                                                                                                                                         397 DDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQL-TPSQQERMLRPSEW 455
                                                                                                                                                                                                                                                                                                                                                                        ||: | | :: | | :: | | : | | 251 DDEDEBEBEBDDDDEBEBEBPVRAAPGRRKK----EMTKQKBAPBAKKQKVEGSE- 304
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                                                                                            316 SSSLSASTSVSDSSQKKEEHNYSLFVSDN------LGEQPTKCSP----EEDEED
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Job time : 238.353 secs
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                                                                                                  NUCLEOTIDE SEQUENCE.
STRAINE-STREINE-SKIN;
STRAINE-STREINE-STREINE,
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/63; TISSUB=Skin;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/6J; TISSUB=Skin,
MDEDLINE=20310913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yoneda Y., Ishikawa T., Ozawa Y., Izawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai Jf.,
Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.,
"RIEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
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llarity 21.0%; Pred. No. 0.053;
Conservative 78; Mismatches 180; Indels 224; Gaps
   "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
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GO; GO:0005730; C:nucleolus; TAS.
InterPro; IPR012677; a b plait nuc_bd.
InterPro; IPR00504; RNP1_RNA_bd.
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SMART; SM00360; RRM; 4.
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adk65805 Angiogene		Adk35935 Novel hum	Human	-		Abg29275 Novel hum			<u>σ</u>	Adf69140 Human MP5	Adq20910 Human sof		Adx05855 Cyclin-de		Aaw81173 Human BAZ		Arabid	Adj46862 Human BIC	Adp55980 Human PRO	Membra	Aau29131 Human PRO	Aab65240 Human PRO	Abu58507 Human PRO
SUMMARIES	ID	ADK65805	ADQ66472	ADK35935	ABP64928	AD020373	ADK65836	ABG29275	ABB04812	AAG84930	AAG85039	ADF69140	ADQ20910	ADX05853	ADX05855	AAW81172	AAW81173	ADH45438	AAG36936	ADJ46862	ADP55980	AAY66717	AAU29131	AAB65240	ABU58507
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Š	ADK65805;
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DE	Angiogenesis-differentially expressed protein ANH0757.
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3	cytostatic; cardiant; vasotropic; antiarteriostationic;
¥	angiogenesis inhibitor; angiogenesis stimulator; angiogenic index;
Ž	gene expression; cancer; coronary artery disease; myocardial ischemia;
Σ	coronary arteriosclerosis; forensic medicine.
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SO	Homo sapiens.
ž	WO2001066831-20
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2	14-AUG-2003.
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PF	07-FEB-2003; 2003WO-US003848.
\$ E	07-FEB-2002; 2002US-00067482.
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A X	(ORIGENE TECHNOLOGIES INC.
I d	Sun Z. Li X. Kovacs KF. Fan W. Jay G;
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DR	WPI; 2003-731502/69.
Ж.	N-PSDB; ADK65804.
ž	notermining the angiousnic index of a tiggue of cell gample using
, t	percentage of differentially expressed dense, useful for
i E	diagnosing or treating cancer, coronary artery disease, myocardial
P.	ischemia and/or arteriosclerosis.
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S X	Claim 23; SEQ ID NO 44; 296pp; English.
{ E	The invention relates to a method of determining the angiogenic index of
35	a tissue or cell sample comprising assessing, in a sample, the expression
8 8	levels of one or more differentially-expressed gene from any of 34 DNA
3 5	samences given in the specification, where the levels are indicative of
36	bequences, given in an operation of the present
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invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary arteriosclerosis. They can also be used in research, drug discovery and forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
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Best Local Similarity 100.
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The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% to 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein sequence of the invention.

Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases. Alzheimer's diseases, Parkinson's diseases, dementia and various cancers

Claim 1; SEQ ID NO 3633; 2449pp; English

ŝ Ishii

Sato H,

Wakamatsu A,

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Otsuki T, Nagai K, I

Sugiyama T, Isono Y,

Yamamoto J,

Isogai T,

2004-535376/52.

N-PSDB; ADQ64284

(REAS-) RES ASSOC BIOTECHNOLOGY 21-JAN-2003; 2003JP-00102206. 09-MAY-2003; 2003JP-00131392. 21-JAN-2004; 2004EP-00001196

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
                                                                                                                                                                                                                                                                                                                                                                                              1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFWYELDREMNYQQNPRDNFL
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                                                                                                                                                                                                                                                                                                                                                        8; Length 417;
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                                                                                                                                                                                                                                                                                                                                                       48.0%; Score 307; DB 8;
99.8%; Pred. No. 4e-290;
tive 0; Mismatches
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Matches 407; Conservative
                                                                                                                                                                                                                                                                                                                                     Sequence 417 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ]
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osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

Homo sapiens

Novel human protein sequence #1445

07-OCT-2004

ADQ66472;

ADQ66472 standard; protein;

ADQ66472

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 SSTQIMVKTNMYHDEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with an antiarthritic, antiparkinsonian, neuroprotective, notropic, immunosuppressive, cytostatic, antiparatic, antiparatic, antiparatic, antiparatic, antinflammatory, introduction, the disclosed sequences may be useful for gene therapy. In polypeptides or their antibodies are useful for treating many diseases such as archritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer, psoriasis, inflammatory bowel disease and infections caused by bacteria, viruses, fungi or parasites. The present sequence is that of a human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 SSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 AVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDS 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 SQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEEEEEE 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
                                                                                                                                                                                                                                                                                                                        /note= "OTHER= All Xaa's in this sequence are unknown amino acids or the site of a stop codon within the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDBEDVDDEDHDEGFGSEHELSENEEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                      antiarthritic; antiparkinsonian; neuroprotective; nootropic; immunosuppressive; cytostatic; antipsoriatic; antiinflammatory; antibacterial; antiviral; antifungal; antiparasitic; gene therapy; arthritis; Parkinson's; Alzhaimer's; autoimmune disease; cancer; psoriasis; inflammatory bowel disease; infection; bacteria; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
31.3%; Score 200; DB 5; Length 256;
Best Local Similarity 100.0%; Pred. No. 6e-186;
Matches 200; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 8017; 504pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treating, e.g., Parkinson's, Alzheim
disease, and inflammatory bowel disease.
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                    Novel human polypeptide SeqID8017.
                                                                                                                                                                                                                                                                                      1. .256
/label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-2000; 2000US-00519705.
19-MAY-2000; 2000US-00574454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAR-2001; 2001WO-US004941
                06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                   sequence
                                                                                                                                                                                       fungus; parasite; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-280918/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 256 AA;
                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                         WO200216439-A2
                                                                                                                                                                                                                               Homo sapiens.
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The present invention relates to novel human coding sequences (ABQ99268-CABQ9608) and proteins (ABP64682-ABP65022). The sequences are useful in therapeutic, diagnostic and research methods. The polymucleotides may be used in the field of molecular biology as hybridisation probes, primers for PCR, for chromosome and gene mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The polymucleotides are useful in diagnostics as expressed sequence tags (BSTS) for identifying expressed genes or for physical mapping of the human genome. The proteins may be used to maintain and expand cell population in a totipotential or pluripotential state and expand cell population in a totipotential or pluripotential state.

Cuseful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals or the development of bio-sensors. The polymucleotides and proteins are useful for preventing or ameliorating disorders involving aberrant protein expression or antiological activity, e.g. haematopoietic disorders, central/peripheral corving, immune disorders involving aberrant protein expression or biological activity, e.g. haematopoietic disorders, central/peripheral corving, immune deficiencies and disorders, infectious diseases caused by viral, bacterial or fungal infection, autoimmune disorders, allergic reactions and conditions, coagulation disorders, or cancer. The coplated mainly by sequencing by hybridisation, and in some cases, cisolated mainly by sequencing by hybridisation, and in some cases, capture of more or more public databases. Note: The sequence data for this patent did not form part of the printed specification, but

New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.

Claim 20; SEQ ID NO 588; 394pp; English.

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Human; expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; peripheral nervous system disease; non-healing wound; infectious disease; immune déficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autrintémune disorder; coaquiation disorder; noctropic; antiallergic; antiinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide;
                                                                                                                                                                                                                                                                                                                                                             V, Zhang J, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                            Tang YI, Goodrich RW, Liu C, Zhou P, Asundi V
Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
                                                                                                                                                                                                                      immunostimulant; cerebroprotective.
                                                                   ABP64928 standard; protein; 168 AA.
          231 EEDYEDDKODDISDTFSEPG 250
EEDYEDDKDDDISDTFSEPG
                                                                                                                                                                                                                                                                                                    16-NOV-2001; 2001WO-US042950.
                                                                                                                                                                                                                                                                                                                      17-NOV-2000; 2000US-00714936.
                                                                                                          25-FEB-2003 (first entry)
                                                                                                                            Human protein SEQ ID 588.
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                                                                                                                                                                                                                                                                                                                                           HYSE- \ HYSEQ INC
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                                                                                                                                                                                                                                                             WO200259260-A2
                                                                                                                                                                                                                                         Homo sapiens
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389
                                                                                       ABP64928;
                                                          ABP64928
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Sequence 296 AA;
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                                                   invention
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                                                                                                                                                             333
                                                                                                                                                                            61 QEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel PRO polypeptide e.g., PRO69614, PRO711106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                               rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic soleroals; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune caleroals; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders in mammals. The immune arthritis, osteoarthritis, juvenile chronic arthritis, systemic arthritis, systemic solores, as arthritis, systemic solores is solores, as arthritis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
                                                                                                                                  1 MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                                                                                                                                               274 QEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKE
                                                                                                            214 MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Human; PRO; immune related disorder; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
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                                                               Length 168;
                                                                                                                                                                                                                           EHNYSLFVSDNLGEQPTKCSPEDEEDEEDVDDEDHDEGFGSEH 164
                                                                                                                                                                                                             EHNYSLFVSDNLGEQPTKCSPEEDEEDVDDEDHDEGFGSEH 377
                                                                                     0, Indels
  at
was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences
                                                            25.7%; Score 164; DB 5; Le 100.0%; Pred. No. 5.4e-151; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; SEQ ID NO 1266; 1731pp; English.
                                                                                                                                                                                                                                                                                                   ADO20373 standard; protein; 296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003; 2003WO-US035268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2002; 2002US-0425235P.
                                                                                                                                                                                                                                                                                                                                                                            Human PRO polypeptide #633
                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                     Matches 164; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spondyloarthropathy
                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu TD;
                                      Sequence 168 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                           ADO20373;
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                                                               Query Match
                                                                            Local
                                                                                                                                                                                                                                                                             RESULT
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mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; cardiant; vasotropic; antiarteriosclerotic; angiogenesis inhibitor; angiogenesis etimulator; angiogenesis cutmulator; angiogenesis cormangene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 MLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 ISDLTPVSELPLTARPRSRKEKNKLASRACRLKKKAQYEANKVKLWGLATEYDNLLFVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 SIKOEIVNRVQNPRDERGFNMGQKLEILIKDTLGLFVAGQTSEFVNQVLEKTAEGNFTGG
                                                                                                                                                                                                                                                                                                                                        389 EEDYEDDKODDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQER
                                                                                                                                                                                                                                                                                                                                                                                         46 EEDYEDDKODDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              509 ISDLTPVSELPLTARPRSRKEKNKLAFRACRLKKKRAQYEANKVKLWGLNTEYDNLLFVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGG
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                         Length 296
                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Angiogenesis-differentially expressed protein #50.
                                                                                                                                                                                                                         Score 150; DB 8;
Pred. No. 4e-137;
0; Mismatches 1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADK65836 standard; protein; 91 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ischemia and/or arteriosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2002; 2002US-00067482.
10-JUN-2002; 2002US-00164595.
16-AUG-2002; 2002US-0403649P.
03-JAN-2003; 2003US-0437746P.
                                                                                                                                                                                                                            23.5%;
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                                                                                                                                                                                                                               Query Match 23.5
Best Local Similarity 99.6
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVGLRIPTSKV 639
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The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary artery disease, myocardial ischemia or coronary or oronary or or also be used in research, drug discovery and forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
8×388888888888888
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Sequence 91 AA;

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508
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                                                                                      1 MLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKV
                                                                    449 MLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKSRRTDVEDLTPNPKKLLQIGNELRKLNKV
                                    0; Gaps
13.0%; Score 83; DB 7; Length 91; 100.0%; Pred. No. 3.1e-72; ive 0; Mismatches 0; Indels
                                                                                                                                            509 ISDLTPVSELPLTARPRSRKEKN 531
                                                                                                                                                            61 ISDLTPVSELPLTARPRSRKEKN 83
                Local Similarity 100.
nes 83; Conservative
   Query Match
                                     Matches
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RESULT 7 ABG29275 원

ABG29275 standard; protein; 160 AA. (first entry) 18-FEB-2002 ABG29275;

n; chromosome mapping; gene mapping; gene therapy; forensic supplement; medical imaging; diagnostic; genetic disorder. Novel human diagnostic protein #29266. WO200175067-A2. Homo sapiens. 11-OCT-2001 food

forensic;

30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

Drmanac RT, Liu C,

WPI; 2001-639362/73. N-PSDB; AAS93462.

Tang YT

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 59634; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed activity of (II) is useful in gene therapy techniques to rescore normal activity of (II) or to treat disease states involving (II) is useful antibodies against it, detecting or quantitating a

The present invention describes a method for detecting a stress that alters a functional interaction of a low density lipoprotein (LDL) (IDL) teceptor interaction domain (II). The method involves introducing a predetermined stress into a system which provides a stress-biased physical interaction of (I) with (II), where in the absence of the stress, the system provides an unbiased interaction of (I) and (II), and detecting the stress-biased interaction of (I) and (II), where a difference between BI and UI indicates that the stress alters the interaction of (I) and (II), where a difference between BI and UI indicates that the SENCAP. JIP., JIP., PSD-95, JIP.2, Tallin, OMP25, CAPON, PIP4,5 Kinase, Na channel brain 3, Mintl, ICAP-1 and APC subunit 10. The method is useful for detecting a stress that alters functional interaction of LDL receptor

Disclosure; Page 78-79; 200pp; English.

domain in a system.

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polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Low density lipoprotein receptor binding protein; signal transduction; LDL receptor binding pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting stress that alters interaction of LDL receptor binding polypeptide with LDL receptor interaction domain, comprises detecting difference in stress-biased and unbiased interaction of peptide and
                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                           Length 160;
                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                  601
                                                                                                                                                                                                                                                                                               29 NLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTL 68
                                                                                                                                                                                                                                                                                   562 NLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTL
                                                                                                                                                                                                                           6.3%; Score 40; DB 4; Lo
100.0%; Pred. No. 4.4e-30;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                  ABB04812 standard; protein; 830 AA
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                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                 Sequence 160 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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Matches
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RESULT 9 AAG84930

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The invention provides the primary nucleotide sequence of the WSBV genome (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences (AAH62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create transgenic viral resistant shrimp. (Updated on 06-AUG-2003 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection.
                                                                                                                                                                                                                                                                                                                                                             Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection; antiviral agent; gene expression; antisense construct; transgenic viral resistant shrimp.
                                                                                                                                                                                                                                                                                                                           Shrimp white spot Bacilliform virus (WSBV) protein 130.
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(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
(SINO-) SINOGENOMAX CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.7%; Score 11; DB 4;
100.0%; Pred. No. 0.48;
ive 0; Mismatches
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                                                                                                                                                                           AAG85039 standard; protein; 1174 AA
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(first entry)
                                                     1000 SENEEEEEEE 1010
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Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200138351-A2.
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11-SEP-2001
                                                                                                                                                                                                                     AAG85039;
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ID ADF6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG8910-AAG88051) and oligomucleotide sequences (AAH62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral agence expression or activity furing a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides the primary nucleotide sequence of the WSBV genome
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binding polypeptide with LDL receptor interaction domain. The method is useful for detecting and modulating signal transduction through LDL receptors. ABB04778 to ABB04909 represent LDL receptor binding proteins which are used in the exemplification of the present invention
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                                                                                                                                                  1.7%; Score 11; DB 5; Length 830;
100.0%; Pred. No. 0.36;
cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shrimp white spot Bacilliform virus (WSBV) protein 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiviral agent; gene expression; antisense construct transgenic viral resistant shrimp.
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(THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
(SINO-) SINOGENOMAX CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-2000; 2000WO-US028888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White spot syndrome virus.
                                                                                                                                                  Query Match 1.7
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                      FNEEEEEEED 104
                                                                                                                                                                                                                                         381 ENEEEEEEED 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
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                                                                                                             Sequence 830 AA;
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11-SEP-2001
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Kodira C;

Shen Y,

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Gaps

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Matches

Length 1174; Indels

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Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; SEQ ID NO 3730; 210pp; English.
                                                                                                                                                                                                      (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                             26-NOV-2002; 2002US-0429739P.
                                                                                                                         26-NOV-2003; 2003WO-US038193.
                                                                                                                                                                                                                                                Aziz N, Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-441208/41.
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                                      WO2004048938-A2
  Homo sapiens.
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                                                                                10-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for identifying a candidate p53 pathway modulating agent, which comprises: (a) providing an assay system comprising a mp53 (modulator of p53) polypeptide or nucleic acid or its cagment or derivative; (b) contacting the assay system with a test agent conditions where the system provides a reference activity except in the presence of the rest agent; and (0) detecting a test agent-biased activity, where a difference between the test agent as a candidate p53 pathway modulating agent; Also described: (1) modulating the p53 pathway in a mammalian cell; and (3) diagnoshing a disease in a patient. Mp53 has cytostatic activity, and can be used in gene therapy. The method is useful for identifying a candidate p53 pathway modulating agent for preparing a composition for diagnosing or treating e.g., cancer. The present sequence represents a human MP53 protein, which is used in the exemplification of the present invention.
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                                                                                                                         p53 pathway modulating agent; MP53; p53 modulator; cytostatic; gene therapy; cancer; human.
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100.0%; Pred. No. 0.59;
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                                                                                    Human MP53 protein sequence SEQ ID NO:110.
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Best Local Similarity 100.
Matches 11; Conservative
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Funke RP;
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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples and comparing the presence of soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and sorcening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
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ive 0; Mismatches
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RESULT 12 ADQ20910 ADQ20910;

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This sequence represents the human BAZ1-beta protein, a member of
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                                                  Biomarkers useful for predicting or determining the response of a mammal to a cancer treatment comprising administration of a modulator of cyclin-
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Pred. No. 0.59;
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                                                                                                      Claim 5; SEQ ID NO 418; 141pp; English
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N-PSDB; ADX05852.
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whether a mammal will respond or in responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more blomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify biomarkers.

The cdk modulator is preferably N5-[[5-(1,1-Dimethylethyl)-2-oxazolyy]methyllthiol-2-thiazolyy-4-piperidine carboxamide, 0.5-Letartaric acid salt. Note: The sequence data for this patent did not form the tenth from WIPO at fitp. Wipo.int/pub/published pot sequences. This sequence represents a biomarker used in the method of the invention.
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                                                                              or determining
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                                                                          invention describes a novel method of predicting
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Claim 5; SEQ ID NO 420; 141pp; English
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CC family of transcriptional regulator genes containing a bromodomain (BAZ, Bromodomain with Atypical Zinc finger) which are expressed specifically CC in testis tissue and also in certain tumour lines. Transgenic cells may CC be used for the preparation of the BAZ1-apha, BAZ1-beta BAZ2-beta and CC BAZ2-beta proteins. These proteins can be used in the treatment of cancer CC and other proliferative disorders, and in screening of compounds for CC their binding ability to the expression products (e.g. for use as drugs CC by modulation of transcriptional regulation)

XX Sequence 1527 AA;
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Query Match 1.7%; Score 11; DB 2; Length 1527; Best Local Similarity 100.0%; Pred. No. 0.61; Matches 11; Conservative 0; Mismatches 0; Indels 0; Qy 383 EEEEEEEEDYE 393

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/f_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-992-598-287
US-10-202-480-2
US-09-792-024-108
US-09-248-796A-17567
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US-09-248-796A-23592
US-09-270-767-41799
US-09-270-767-57041
US-10-202-480-4
US-09-991-181-287
US-09-990-444-287
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US-09-839-479-27
US-09-418-710-29
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US-09-976-740-25
US-08-979-608A-26
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                                                                                                                                                                                           572060 segs, 82675679 residues
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                                            OM protein - protein search, using sw model
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639
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Maximum DB seq length: 200000000
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Match Length DB
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US-09-616-289-26 US-09-976-740-26 US-09-976-740-26 US-09-018-678-33 US-09-912-962-33 US-09-513-999C-6304 US-09-513-999C-6304 US-09-621-976-5741 US-08-52-142A-9 US-08-910-973-9 US-08-910-973-9 US-08-910-973-9 US-08-910-973-9 US-09-248-786A-14111	US-09-702-705-324 US-09-702-705-789 US-09-736-457-324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 SPLPQEGPGSLAAGESSSLSASTSVSDSSQXKEEHNYSLFVSDNLGEQPTKCSPEDDED 360
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Sequence 44, Application US/10164595

Patent No. 6657054

GENERAL INFORMATION:

APPLICANT: Origine Technologies, Inc.

TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides

FILE REFERENCE: 1U 103 R1

CURRENT APPLICATION NUMBER: US/10/164,595

CURRENT APPLICATION NUMBER: US/10/164,595

CURRENT FILING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn version 3.1

SEQ ID NO 44

LENGTH: 639
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100.0%; Pred. No. 0;
ative 0; Mismatches
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Best Local Similarity 100.
Matches 639; Conservative
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) ORGANISM: Homo sapiens
US-09-839-479-68
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                   381
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                     RRTDVEDLTPNPKKLLQIGNELRKLNKVISDLTPVSELPLTARPRSRKEKNKLAFRACRL 540
                                                                                                                                                              KKKAQYEANKVKLWGINTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDT 600
                                                                                                                                                                                     541 KKKAQYEANKVKLMGINTEYDNILFYINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDT 600
TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS 480
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TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REPERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3:1
SEQ ID NO 75
LENGTH: 91
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
ISOURCE INFORMATION: Sequence
US-09-562-737-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.0%; Score 83; DB 2; Length 91; 100.0%; Pred. No. 1.4e-70; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 601 LGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 639
                                                                                                                                                                                                                                                                                     601 LGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 639
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APPLICANT: Herz, Joachim
APPLICANT: Getthardt, Michael
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 35
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Patent No. 6657054
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Patent No. 6428967
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ORGANISM: Artificial Sequence
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; ORGANISM: Homo sapiens
US-10-164-595-75
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                           TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR ITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR PLIE REPERENCE: 06501-042001
CURRENT APPLICATION NUMBER: U$/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-839-479-68

j Sequence 68, Application US/09839479

patent No. 6727222

GENERAL INFORMATION:
   APPLICANT JONES, Michael H.
   TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
   FILE REFERENCE: 06501-042002

CURRENT APPLICATION NUMBER: US/09/839,479

CURRENT FILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: PCT/JP98/01783

PRIOR PILING DATE: 1999-10-15

PRIOR PILING DATE: 1999-10-15

PRIOR PILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: DP 9/310027

PRIOR APPLICATION NUMBER: JP 9/310027

PRIOR APPLICATION NUMBER: JP 9/310627

PRIOR FILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FRASERO FOR Windows Version 4.0

SEQ ID NOS: 72
                                                                                          US-09-418-710-69; Sequence 69, Application US/09418710; Patent No. 6596482; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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94 ENEEEEEEED 104
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Sequence 7037, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.25;
cive 0; Mismatches
                nes, Michael H.
TION: TRANSCRIPTIONAL REGULATOR
              APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATON
FILE REPERENCE: 06501-042001
CURRENT APPLICATION NUMBER: U5/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR PELLING DATE: 1998-64-17
PRIOR PELLING DATE: 1998-04-17
PRIOR PELLING DATE: 1997-10-24
PRIOR PELLING DATE: 1997-10-24
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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US-09-839-479-29
                                                                                                                                                                                                                                                                                               ; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-29
GENERAL INFORMATION:
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US-09-949-016-7037
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TYPE: PRT
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                                                                                                                                                                                                                                                                           SEQ ID NO 29
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.7%; Score 11; DB 2; Length 1527; Best Local Similarity 100.0%; Pred. No. 0.25; Matches 11; Conservative 0; Mismatches 0; Indels
                                                   Sequence 27, Application US/09418710

Sequence 27, Application US/09418710

Patent No. 6566482

GENERAL INFORMATION:

TATLE OF INVENTION: TRANSCRIPTIONAL REGULATOR;

FILE REFERENCE: 66501-64201

CURRENT APPLICATION NUMBER: US/09/418,710

CURRENT FILING DATE: 1999-10-15;

PRIOR APPLICATION NUMBER: DET/JP98/01783

PRIOR PILING DATE: 1999-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 73

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 27

LENGTH: 1527

TYPE: PRI

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: JOHES, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT PILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: US/09/418,710
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: UP 9/310027
PRIOR APPLICATION NUMBER: UP 9/310027
PRIOR APPLICATION NUMBER: UP 9/310027
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
SEQ ID NO 27
LENGTH: 1527
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; Sequence 29, Application US/09418710
; Patent No. 6596482
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Patent No. 6727222
GENERAL INFORMATION:
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                                           US-09-418-710-27
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TYPE: PRT

Query Match

RESULT 8

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Sequence 4, Application US/10202480

Facent No. 623923

GENERAL INFORMATION:
APPLICANT: Vallone, Marcy K.
APPLICANT: Wong, Brian R.
APPLICANT: Masuda, Esteban
APPLICANT: Modulators of Leukocyte Activation, BIC Compositions and Methods of TITLE OF INVENTION: Modulators of Leukocyte Activation, BIC Compositions and Methods of TITLE OF INVENTION: Modulators of Leukocyte Activation, BIC Compositions and Methods of TITLE OF INVENTION: Modulators of Leukocyte Activation, BIC Compositions and Methods of CURRENT APPLICATION NUMBER: US/10/202,480
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                       RESULT 13
US-09-270-767-57041
; Sequence 57041, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 625.7
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 57041
; LENGTH: 141
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100.0%; Pred. No. 0.41;
tive 0; Mismatches 0; Indels
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                               Length 141;
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                            1.6%; Score 10; DB 2;
100.0%; Pred. No. 0.26;
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US-09-991-181-287
; Sequence 287, Application US/09991181
; Patent No. 6913919
; GRUERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 10; Conservative
                               Query Match
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                    39 RACRLKKKAQ 48
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US-10-202-480-4
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Reith Weinstock et al
APPLICANT: Reith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 23592
LENGTH: 114
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7226-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41799
LENGTH: 141
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100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
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0.22;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 7037
LENGTH: 1540
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US-062-248-796A-23592
; Sequence 23592, Application US/09248796A
; Patent No. 6747137
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Sequence 41799, Application US/09270767
Perent No. 6703491
GENERAL INFORMATION:
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US-09-270-767-41799
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; ORGANISM: Candida albicans
US-09-248-796A-23592
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Matches 11; Conservative
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; ORGANISM: Human
US-09-949-016-7037
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FILING DATE: 1998-06-05
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
TLE REFERENCE: P2730P1C53
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 05/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR PHILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06226
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
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R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/083322
R FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087609
R PILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/087759
R FILING DATE: 1998-06-02
R FILING DATE: 1998-06-03
R FILING DATE: 1998-06-03
R APPLICATION NUMBER: 60/088021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25
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FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/066770
                                                                                                                                                                  Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                  Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                  Ferrara, Napoleone
Fong, Sherman
Gerber, Hanspeter
                                                                                                                                                                                                                                                 Paoni, Nicholas F.
                                                                                                                  Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                   Godowski, Paul J.
                    Botstein, David
                                                                                                                                                                                                                  Napier, Mary A.
      Baker, Kevin P
                                     Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                     Рап, Јашев
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      APPLICANT
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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088624
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/08826
R APPLICATION NUMBER: 60/08826
R APPLICATION NUMBER: 60/08828
R APPLICATION NUMBER: 60/08888
R APPLICATION NUMBER: 60/088881
R APPLICATION NUMBER: 60/08881
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-19
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LING DATE: 1998-06-17
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ILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089907
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                        FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/080810
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FILING DATE: 1998-06-12
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FLING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088202
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Query Match
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Matches 10; Conservative 0; Mismatches 0; Indels

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Sequence 35, Appl
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Sequence 287, App Sequence 287, App		and Polypeptides	Length 639; ; Indels 0; Gaps 0;	PDFMYELDREMNYQQNPRDNFL 60	TKYTKLTSCDIWGTKEVDYLGL 120 TKYTKLTSCDIWGTKEVDYLGL 120	SLFSVKQNPLPSSFPGKKITSR 180 	QIMVKTNMYHNEKVNFHVECKDYVKKAKV 240
255 3 US-09-989-721-287 255 3 US-09-992-598-287 255 3 US-09-992-593A-287 255 3 US-09-999-735-287 255 3 US-09-990-735-287 255 3 US-09-991 181-287 255 3 US-09-991 730-287 255 3 US-09-991 730-287 255 3 US-09-997-734-287 255 3 US-09-997-687-287 255 3 US-09-993-687-287 255 3 US-09-993-687-287 255 3 US-09-993-687-287 255 3 US-09-997-28-287 255 3 US-09-997-28-287 255 3 US-09-997-428-287	ALIGNMENTS	17665 s, Inc Anglogenesis Genes /10/717,665 21 0/164,595	100.0%; Score 639; DB 5; 100.0%; Pred. No. 0; ative 0; Mismatches 0.	SEQTLMSTDLLANSSD 	SLEDCKDIENLESFTDVLDNEGALTSNWEGWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL 	DDFSSPYQDEEVISKTPTLAQLASEDSQSVSDSLYXPDSLFSVKQNPLPSSFPGKK.TSR 	AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
		SULT 1 10-717-665-44 Sequence 44, Application US/10717665 Publication No. US20050106579A1 GENERAL INFORMATION: APPLICANT: OriGene Technologies, Inc TITLE OF INVENTION: Regulated Angloge FILE REFERENCE: 1U 103 R1 CURRENT FILING DATE: 2003-11-21 PRIOR APPLICATION NUMBER: US/10/717 CURRENT FILING DATE: 2003-11-21 PRIOR FILING DATE: 2002-06-10 NUMBER OF SEQ ID NOS: 80 SOFTWARE: PATHLING DATE: 2002-06-10 NUMBER OF SEQ ID NOS: 80 IENGTH: 639 TYPE: PRT ORGANISM: HOMO SADIENS	atch cal Similarity 639; Conservat	1 MPQPSVSGMDPPFGDAFRSHTF 	61 SLEDCKDIENLE 	121 DDFSSPYQDEEVI 121 DDFSSPYQDEEVI	181 AAAPVCSSKTLQ 181 AAAPVCSSKTLQ
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Publication No. US2005010657941
GENERAL INFORMATION:
APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US/10/11,665
PRIOR FILING DATE: 2002-06-10
PRIOR FILING DATE: 2002-06-10
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: HYSEQ.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT PILICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR PILING DATE: 2001-03-30
; PRIOR PLING DATE: 2000-03-31
; PRIOR PLING DATE: 2000-03-31
; PRIOR PLING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: CUSTOM
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13.0%; Score 83; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 9.4e-70;
Matches 83; Conservative 0; Mismatches 0;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-10-717-665-75
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Sequence 3730, Application US/10723860
; Sequence 3730, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
    APPLICANT: Aliable APPLICANT: Clinburg, Wendy M.
; APPLICANT: Zlornik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Modulators
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Modulators
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Modulators
; PRIOR PLILING DATE: 2003-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
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Length 160;
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APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REPERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/10/211,962
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US/09/562,737
PRIOR APPLICATION NUMBER: US/09/562,737
NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
                                                                                                                      562 NLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTL
DB 5; Le
5.7e-29;
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100.0%; Pred. No. 0.55;
tive 0; Mismatches
Query Match 6.3%; Score 40; DB Best Local Similarity 100.0%; Pred. No. 5.7 Matches 40; Conservative 0; Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11, Conservative
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US-10-723-860-3730
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LENGTH: 830.
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100.0%; Pred. No. 0.94;
tive 0; Mismatches 0; Indels
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US-10-3/6-53/-69

Publication No. US20030224405A1

GENERAL INPORMATION:
APPLICANT: JORGE, MICHAEL H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFRENCE: 06501-042001
CURRENT APPLICATION NUMBER: US/09/418,710

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-04-18

NUMBER OF SEQ 1D NOS: 73

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 1525

TYPE: PRIOR FILING DATE: 1997-04-18
                                                                                                                   Sequence 68, Application US/09839479
Publication No. US20020039779A1
GENERAL INPORMATION:
APPLICANT: JONES, Michael H.
TILLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042002
                                                                                                                                                                                                                                      TLLE KEKEKEREL 1053-L042-02.09

CURRENT APPLICATION NUMBER: US/09/839,479

CURRENT FILING DATE: 2001-04-20

PRIOR APPLICATION NUMBER: US 09/418,710

PRIOR PILING DATE: 1999-10-15

PRIOR PILING DATE: 1999-10-15

PRIOR PILING DATE: 1998-04-17

PRIOR FILING DATE: 1999-10-24

PRIOR PILING DATE: 1997-04-18

PRIOR APPLICATION NUMBER: UP 9/116570

PRIOR PILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 68

LENGTH: 1525
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Best Local Similarity 100.
Matches 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
1266 REEEEEBBDYE 1276
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US-10-376-537-69
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ORGANISM: Homo sapiens
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                                                                                                        -09-839-479-68
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US-10-702-148-68

US-10-702-148-68

Sequence 68, Application US/10702148

Publication No. US20040063145A1

GENERAL INFORMATION:

APPLICATION NO. US20040063145A1

GENERAL INFORMATION:

TILLE OF INVENTION: TRANSCRIPTIONAL REGULATOR

FILE REFERENCE: 66501-042002

CURRENT PILING DATE: 2003-11-05

CURRENT PILING DATE: 2003-11-05

PRIOR FILING DATE: 2001-04-20

PRIOR PILING DATE: 1999-10-15

PRIOR PELING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: PCT/JP98/01783

PRIOR APPLICATION NUMBER: PCT/JP98/01783

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH. 15-05
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100.0%; Pred. No. 0.94;
tive 0; Mismatches 0; Indel8
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100.0%; Pred. No. 0.94;
ive 0; Mismatches 0; Indels
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Publication No. US20020039779A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 11; Conservative
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TYPE: PRT
CRGANISM: Homo sapiens
US-09-839-479-27
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US-10-702-148-68
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Matches 11; Conserva
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US-09-839-479-27
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Homo sapiens
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US-10-702-148-27
Sequence 27, Application US/10702148
Publication No. US20040063145A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: TRANSCRIPTIONAL RECULATOR
TITLE OF INVENTION:
FILE REFERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/10/702,148
CURRENT FILING DATE: 2003-11-05
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: US/310027
PRIOR APPLICATION NUMBER: US/99/10-24
PRIOR APPLICATION NUMBER: US/99/10-24
PRIOR APPLICATION NUMBER: US/99/10-24
PRIOR APPLICATION NUMBER: US/10-24
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100.0%; Pred. No. 0.94;
cive 0; Mismatches 0; Indels
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                    PUBLICATOR APPLICATION US/10376537
PUBLICATION NO. US20030224405A1
GENERAL INFORMATION.
GENERAL INFORMATION: TRANSCRIPTIONAL REGULATOR
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
CURRENT APPLICATION NUMBER: US/10/376,537
CURRENT PILING DATE: 2003-02-28
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-417
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR APPLICATION NUMBER: JP99/110027
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FASTESEQ FOR WINDOWS VERSION 4.0
IENGTH: 1527
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Matches 11; Conservative
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; ORGANISM: Homo sapiens
US-10-376-537-27
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US-10-702-148-27
-10-376-537-27
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Sequence 29, Application US/10376537

Publication No. US20030224405A1

GENERAL INFORMATION:

APPLICANT: Jones Michael H.

TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR

FILE REFERENCE: 06501-042001

CURRENT APPLICATION NUMBER: US/09/418,710

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: PCT/JP98/01783

PRIOR APPLICATION NUMBER: PCT/JP98/01783

PRIOR APPLICATION NUMBER: US/9/310027

PRIOR APPLICATION NUMBER: US/9/116570

PRIOR PILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 73

SEQ ID NO 29

LENGTH: 1531
Publication No. US2002003977941

GENERAL INFORMATION:
APPLICANT: JONES, MICHAEL H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REPRENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/819,479
CURRENT FILING DATE: 2001-04-20
FRIOR PILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1997-10-24
FRIOR APPLICATION NUMBER: UP 9/310027
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
FRIOR FILING DATE: 1997-04-18
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FRIOR FILING DATE: 1997-04-18
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Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 11; Conservative 0; Mismatches (
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US-10-702-148-29
Sequence 29, Application US/10702148
Publication No. US20040063145A1
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; ORGANISM: Homo sapiens
US-09-839-479-29
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RESULT 15
US-10-425-115-204867
Sequence 204867, Application US/10425115
Sequence 204867, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Lou, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)
CURRENT FILING DATE: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/425,115
SEQ ID NO 204867
LEMOTH: 102
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GENERAL INFORMATION:

APPLICANT: JONES, Michael H.

IITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR

FILE REPERBNCE: 06501-042002

CURRENT APPLICATION NUMBER: US/10/702,148

CURRENT PILING DATE: 2003-11-05

PRIOR PELING DATE: 2001-04-20

PRIOR PELING DATE: 1999-10-15

PRIOR PELING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: US 09/418,710

PRIOR PILING DATE: 1999-10-15

PRIOR PILING DATE: 1999-04-17

PRIOR PELING DATE: 1999-10-24

PRIOR PELING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PRESEQ for Windows Version 4.0

SEQ ID NO 29

LENGTH: 1531
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100.0%; Pred. No. 0.94;
trive 0; Mismatches 0; Indels
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US-10-425-115-204867
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Matches 11; Conservative
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GRGANISM: Homo sapiens
US-10-702-148-29
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ORGANISM: Zea mays
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Search completed: February 28, 2006, 09:14:18 Job time : 167 secs

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385 EEEEEEDYED 394
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US-11-040-488-2
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LENGTH: 593
TYPE: PRT
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Sequence 308, App
Sequence 16, Appl
Sequence 45, Appl
Sequence 29, Appl
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Sequence 74
Sequence 34
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2: /cgn2 6/ptodata/2/pubpaa/USO6_NEW—PUB.pep:*
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4: /cgn2 6/ptodata/2/pubpaa/NSO7 NEW PUB.pep:*
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6: /cgn2 6/ptodata/2/pubpaa/USO9 NEW PUB.pep:*
7: /cgn2 6/ptodata/2/pubpaa/USO1 NEW—PUB.pep:*
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                           GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
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US-11-098-686-10232
US-10-821-234-1345
US-10-821-234-1254
US-11-067-425A-71
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US-10-821-234-1170
US-10-714-887-122
US-11-072-512-3096
US-11-072-512-3843
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US-11-126-313-31
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                    Sequence:
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26 B 1.3 354 7 US-11-189-817-2 Sequence 2, Appli 29 B 1.3 364 7 US-11-124-367A-309 Sequence 1536, App 29 B 1.3 447 6 US-10-54-385-4 Sequence 1536, App 29 B 1.3 454 6 US-10-569-385-4 Sequence 1536, App 31 8 1.3 457 6 US-10-592-545-8 Sequence 13, Appli 31 8 1.3 457 6 US-10-982-545-8 Sequence 13, Appli 31 8 1.3 457 6 US-10-982-545-13 Sequence 13, Appli 31 8 1.3 565 7 US-10-508-263-20 Sequence 13, Appli 31 8 1.3 565 7 US-11-236-198-19 Sequence 10, Appli 31 8 1.3 565 7 US-11-236-198-19 Sequence 10, Appli 32 8 1.3 565 7 US-11-236-198-19 Sequence 10, Appli 32 8 1.3 565 7 US-11-236-198-19 Sequence 10, Appli 32 56 7 US-11-236-198-19 Sequence 10, Appli 32 56 7 US-11-236-198-19 Sequence 10, Appli 32 56 7 US-11-236-198-19 Sequence 10, Appli 33 56 7 US-11-236-198-19 Sequence 10, Appli 41 8 1.3 546 7 US-11-236-198-17 Sequence 2103, Appli 42 8 1.3 605 6 US-10-31-826A-42 Sequence 216, Appli 43 8 1.3 642 6 US-10-31-826A-285 Sequence 2366, Appli 44 8 1.3 642 6 US-10-131-826A-370 Sequence 370, Appli 45 B 1.3 642 6 US-10-131-826A-370 Sequence 370, Appli 45 B 1.3 642 6 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-370 Sequence 370, Appli 45 US-10-131-826A-
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RESULT 1

US-11-040-488-2.

US-11-040-488-2.

I SEQUENCE 2, PAPPLICATION US/11040488

PUBLICANT. WEBB, CARD.

TITLE OF INVENTION: EXCESSIVE IMMUNOGLOBULIN PRODUCTION

FILLE REFERENCE: OMF: 02213

CURRENT PILLING DATE: 2005-01-21

CURRENT PILLING DATE: 2005-01-21

PRIOR PILLING DATE: 2005-01-23

CURRENT PILLING DATE: 2005-01-23

PRIOR PILLING DATE: 2005-01-23

PRIOR PILLING DATE: 2005-01-23

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PRESENCE: 2005-01-23
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Sequence 1170, Application US/10821234
Publication No. US20050255114A1
Publication No. US20050255114A1
Publication No. US20050255114A1
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia FILE REFERENCE: 821A
CURRENT APPLICANTION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
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APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKWA, TSUTOMU
APPLICANT: NACHIKWA, TSUTOMU
APPLICANT: NACHARA, KENJI
APPLICANT: NACHARA, KENJI
APPLICANT: NACHARA, KENJI
APPLICANT: NASUHO, YASUHIKO
TITLE OF INVENTION: NOVel full length CDNA
FILE REFERENCE: 084335-0191
CURRENT FILING DATE: 2005-03-07
PRIOR FILING DATE: 2005-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3158
LENGTHARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.4%; Score 9; DB 7
Best Local Similarity 100.0%; Pred. No. 0.4
Matches 9; Conservative 0; Mismatches
  Mismatches
                                                                                                                                                            US-11-072-512-3158; Application US/11072512; Sequence 3158; Application OS/11072512; Publication No. US20060029945A1; GENERAL INFORMATION: APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1170
  ..
0
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SUGIXAMA, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAMECHIKA, ICHIRO
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NAGAI, KEIICHI
IRIE, RYOTARO
9; Conservative
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                                         359 EDEEDVDDE 367
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APPLICANT:
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  Matches
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Squence 74, Application US/11067425A

Squence 74, Application US/11067425A

Publication No. US20050278803A1

GENERAL INFORMATION:

APPLICANT: Hannoufa, Abdelali

APPLICANT: Lydiate, Derek J.

APPLICANT: Gao, Ming-Jun

TITLE OF INTERTION REGULATION OF GENE EXPRESSION USING CHROMATIN REMODELLING FACTORS

TITLE OF INTERTION NUMBER: US/11/067, 425A

CURRENT FILING DATE: 2005-02-22

PRIOR APPLICATION NUMBER: US 10/516,753

PRIOR PPLICATION NUMBER: PT/CA03/00822

PRIOR APPLICATION NUMBER: US 60/387,088

PRIOR APPLICATION NUMBER: US 60/387,088

PRIOR PPLING DATE: 2002-06-06

NUMBER OF SEQ ID NOS: 108

SEQ ID NO 74

LENGTH: 221
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; Sequence 34, Application US/11063343
; Publication No. US20050272061A1
; GENERAL INFORMATION:
; APPLICANT: Petroziello, Joseph M.
APPLICANT: Carter, Paul
; TITLE OF INVENTION: Expression Profiling in Non-Small Cell
; TITLE OF INVENTION: Lung Cancer
; FILE REFERENCE: 26811-003N
; CURRENT APPLICATION NUMBER: US/11/063,343
; CURRENT FILING DATE: 2005-02-22
; PRIOR FILING DATE: 2004-02-19
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.4%; Score 9; DB 7; Length 229; PBet Local Similarity 100.0%; Pred. No. 0.36;
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                                                                                                      Length 215;
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                                                                                                      Query Match

1.4%; Score 9; DB 6
Best Local Similarity 100.0%; Pred. No. 0.3
Matches 9; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 0.3
Matches 9; Conservative 0; Mismatches
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188 EEDEEDEED 196
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ORGANISM: Homo sapiens
  ; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
; ORGANISM: Arabidopsis
US-11-067-425A-74
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Sequence 122, Application US/10714887

Publicarion No. 102006001597A1

GENERAL INFORMATION:
APPLICANT: Herako, Jacqueline
APPLICANT: Herako, Jacqueline
APPLICANT: HERAKO, Jacqueline
APPLICANT: MICCIPRE, Oliver
APPLICANT: MICCIPRE, Oliver
APPLICANT: GENERALA, Robert
APPLICANT: GENERAL, Robert
APPLICANT: GENERAL, Robert
APPLICANT: MINIOTO, Roderick W
APPLICANT: FREEFIX, Noilver
APPLICANT: FREEFIX, SROGER
APPLICANT: FREEFIX, SROGER
APPLICANT: FRIENCY, Noilver
APPLICANT: MINIOTO, Roderick W
APPLICANT: MINIOTO, Roderick W
APPLICANT: MINIOTO, Robert
APPLICANT: MINIOTO, Robert
APPLICANT: MINIOTO, Robert
APPLICANT: MINIOTO, Robert
APPLICANT: MINIOTO, Robert
APPLICANTON NUMBER: 105/10/114, 887
CURRENT FILING DATE: 2003-101-13
FRIOR FILING DATE: 2003-101-10
FRIOR PELING DATE: 2003-101-10
FRIOR PELING DATE: 3000-02-17
FRIOR PELING DATE: 3000-02-17
FRIOR PELING DATE: 3000-02-17
FRIOR APPLICATION NUMBER: 09/533, 392
FRIOR FILING DATE: 3000-03-22
FRIOR PELING DATE: 2000-03-22
FRIOR APPLICATION NUMBER: 09/533, 303
FRIOR PELING DATE: 2000-03-22
FRIOR APPLICATION NUMBER: 09/533, 303
FRIOR PELING DATE: 2000-03-22
FRIOR PELING DATE: 2000-03-22
FRIOR PELING DATE: 2000-03-22
FRIOR PELING DATE: 2000-03-17
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US-10-714-887-122
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                                                                                                                                                      Length 414;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Oryza sativa (japonica cultivar-group)
                                                                                                                                                Query Match
1.4%; Score 9; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                               383 EEEEEEED 391
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1170
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NACAHARI, KENII
APPLICANT: NACAHARI, KENII
APPLICANT: NASHGO, YASUHIKO
TITLE OF INVANTION: Novel full length cDNA
FILE REPRENCE: 08435-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT APPLICATION NUMBER: US 60/350,978
PRIOR PRIOR APPLICATION NUMBER: UP 2001-379298
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PACHILIN Ver. 2.1
SOFTWARE: PACHILIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3843, Application US/11072512;
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: SCGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: STRIKT, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: SHII, SHIZUKO
APPLICANT: ISHII, SHIZUKO
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: HOO, YURI
APPLICANT: HOO, YURI
APPLICANT: HOO, YURI
APPLICANT: IRIE, RYOTARO
Sequence 3096, Application US/11072512 Publication No. US20060029945A1 GENERAL INFORMATION:
                                                              APPLICANT: 150GAI, TAKAO
APPLICANT: 5UGIYAWA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                  OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NACHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
MASUHO, YASUHIKO
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-11-072-512-3096
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APPLICANT:
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AND SELECT

383 EEEEEEED 391

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12 EEEEBEED 20

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Sequence 31, Application US/11126313
Publication No. US20050288489A1
GENERAL INFORMATION:
APPLICANT HISTON.
TITLE OF INVENTION: VOLTAGE-DEPENDENT CALCIUM CHANNEL BETA SUBUNIT FUNCTIONAL CORE
FILE REFERENCE: P-6758-US
CURRENT APPLICATION NUMBER: US/11/126,313
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APPLICANT: MICRALIDA:
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-240CIP
CURRENT APPLICATION NUMBER: 05/11/054,281
CURRENT FILING DATE: 2005-02-08
FRIOR PILING DATE: 2001-01-11
FRIOR APPLICATION NUMBER: 60/261,018
FRIOR PILING DATE: 2001-01-11
FRIOR APPLICATION NUMBER: 60/261,013
FRIOR PILING DATE: 2001-01-11
FRIOR APPLICATION NUMBER: 60/261,026
FRIOR APPLICATION NUMBER: 60/261,026
FRIOR PILING DATE: 2001-01-11
FRIOR PILING DATE: 2001-01-11
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FRIOR PILING DATE: 2001-01-11
FRIOR PILING DATE: 2001-01-11
FRIOR FILING DATE: 2002-01-11
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1.4%; Score 9; DB 7;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches
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                                                                                                                                                                                              ; LOCATION: (1)...(1178) at all Xaa position; OTHER INFORMATION: Xaa = any amino acid US-11-044-899-29
  NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
LENGTH: 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 107, Application US/11054281 Publication No. US20060013813A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Rattus norvegicus
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                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                 NAME/KEY: VARIANT
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US-11-054-281-107
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Publication No. US20050260616A1
GENERAL INFORMATION:
APPLICANT: Schwab, M.
APPLICANT: Schwab, M.
APPLICANT: Chen, M.
TITLE OF INVENTION: THEREON
FILE OF INVENTION: THEREON
FILE OF INVENTION: THEREON
FILE OF INVENTION: THEREON
FILE OF INVENTION: UNMBER: US/11/044,899
CURRENT FILING DATE: 2005-01-26
PRIOR APPLICATION NUMBER: 09/830,972
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-05
PRIOR FILING DATE: 1999-11-06
PRIOR FILING DATE: 1999-11-06
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100.0%; Pred. No. 1;
tive 0; Mismatches
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100.0%; Pred. No. 1.1;
tive 0; Mismatches
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT TAPLICATION NUMBER: US/11/072,512
FRIOR APPLICATION NUMBER: US 60/350,978
FRIOR FILING DATE: 2002-01-25
FRIOR FILING DATE: 2002-01-379298
FRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENT NOS: 4096
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-11.078-189-14

Sequence 14, Application US/11078189

Sequence 14, Application US/11078189

Publication No. US20050277167A1

GENERAL INFORMATION:

APPLICANT: Bachinger, Hans Peter

APPLICANT: Vranka, Janice

TITLE OF INVENTION: PROLYL 3-HYDROXYLASES

FILE REFERENCE: 08062-020001

CURRENT APPLICATION NUMBER: US/11/078,189

CURRENT FILING DATE: 2005-03-11

PRIOR APPLICATION NUMBER: US 60/552,409

PRIOR FILING DATE: 2004-03-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14
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Matches 9; Conservative
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253 EEEEEEED 261
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
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US-11-044-899-29
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Publication No. U320060024696A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND FOLYPEPTIDE SEQUENCES
TITLE OF INVENTION: WUCLEIC ACID AND FOLYPEPTIDE SEQUENCES
TITLE OF INVENTION: PROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR PILING DATE: 2003-10-04

NUMBER: OF SEQ 1D NOS: 11433
SOFTWARE: FRSEEE FASTESEQ for Windows Version 4.0
SEQ 1D NO 10232
LENGTH, 8746
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US-11-044-111-24

J Sequence 24, Application US/11044111

Publication No. US20050272362A1

GENERAL INFORMATION:

APPLICANT: Chiang, Wen

APPLICANT: Linz, John

TITLE OF INVERTION: Genetic Test for PSE-Susceptible Turkeys

TITLE OF INVERTION: Genetic Test for PSE-Susceptible Turkeys

CURRENT APPLICATION UNDER: US/11/044,111

CURRENT APPLICATION UNDER: US/11/044,111

SOFTWARR: PatentIn version 3.3

SEQ ID NO 24

LENGTH: 4868

TYPE: PRT

ORGANISM: Meleagris gallopavo

US-11-044-111-24
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1.4%; Score 9; DB 7; Length 8746;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels
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1.4%; Score 9; DB 7; Length 4868;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels
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1.4%; Score 9; DB 7; Length 2161;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels
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; ORGANISM: Lawsonia intracellularis
US-11-098-686-10232
CURRENT FILING DATE: 2005-05-11 NUMBER OF SEQ 1D NOS: 38 SOFTWARE: Patentin version 3.3 SEQ 1D NO 31 LENGTH: 2161
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                                                                                                                 TYPE: PRT
ORGANISM: homo sapiens
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US-11-098-686-10232
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Qy 391 DYEDDKDDD 399
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| Db 2370 DYEDDKDDD 2378
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Search completed: February 28, 2006, 09:27:39 Job time : 20 secs

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639
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                                                                                                             February 28, 2006, 09:06:06; Search time 42 Seconds
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                           OM protein - protein search, using sw model
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A26630
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Maximum DB seq length: 200000000
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Score Match Length DB
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## ALIGNMENTS

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A;Cross-references: UNIPARC:UPI000007CD27; EMBL:283239; PIDN:CAB05811.1; GSPDB:GN00023; (A;Experimental source: clone T09F5
                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Reaidues: 1-517 <MIL>
A;Cross-references: UNIPROT:017941; UNIPARC:UPI00007CD27; EMBL:Z81099; PIDN:CAB03189.1;
A;Experimental source: clone K08F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                        hypothetical protein KO8F9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Spacession: T23499; T24766
R;Mortimore, B.
Submitted to the EMBL Data Library, October 1996
A;Reference number: Z19748
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A;Introns: 16/2; 44/2; 66/2; 277/2; 341/3; 410/2; 426/3
C;Superfamily: Caenorhabditis elegans hypothetical protein K08F9.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 1.7%; Score 11; DB 2; Length 517; 1 Similarity 100.0%; Pred. No. 0.017; 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       R;Mortimore, B.

Bubmitted to the EMBL Data Library, December 1996
A;Reference number: 21993
A;Accession: T24766
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-517 <WI2>
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Matches 11; Conserv
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RESULT 1
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Transcription regulator WBSCR9 - mouse
NyAlternate names: Williams-Beuren syndrome deletion transcript 9 homolog
CyAlternate names: Williams-Beuren syndrome deletion transcript 9 homolog
CySpecies: Mus musculus (house mouse)
CyBate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CyAccession: T1401
RyPeoples, R.J.; Cisco, M.J.; Kaplan, P.; Francke, U.
Cytogenet. Cell Genet. 82, 238-246, 1998
Ayritle: Identification of the WBSCR9 gene, encoding a novel transcriptional regulator, i
AyReference number: 218735; MUID:99077764; PMID:9858827
A.Accession: T17401
A;Status: preliminary; translated from GB/EMBL/DDBJ

RESULT T17401

high mobility grou nonhistone chromos nonhistone chromos

S54774 NSRTH1

nonhistone chromos non-histone chromo hypothetical prote nonhistone chromos

nonhistone chromos

hypothetical prote

Tue Feb 28 11:30:09 2006

C,Genetics:

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N;Contains: progesterone receptor form A
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: A33466; S06284; A40903; A24661; A40312; A40911; A61552
R;Jeltsch, J.M.; Turcotte, B.; Garnier, J.M.; Lerouge, T.; Krozowski, Z.; Gronemeyer, H.; J. Biol. Chem. 265, 3867-3974, 1990
A;Title: Characterization of multiple mRNAs originating from the chicken progesterone rec A;Reference number: A35466; MUID:90154085; PMID:2303488
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A; Title: Sequence and expression of a functional chicken progesterone receptor.
A; Reference number: A40903; MUID:91042592; PMID:3153474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Mesiduse: 128-133, Fz, 135-147, Fz, 149-164 <CO2>
A; Residuse: 128-133, Fz, 135-147, Fz, 149-164 <CO2>
A; Cross-references: UNIPARC:UPI0000177COA
A; Note: the authors translated the codon CAG for residue 7 as Glu and CAG for residue 21
A; Note: the authors translated the codon CAG for residue 7 as Glu and CAG for residue 21
A; Note: the authors translated the codon CAG for residue 7 as Glu and CAG for residue 21
Proc. Natl. Acad. Sci. U.S.A. 83, 5424-5428, 1986
A; Title: Cloning of the chicken progesterone receptor.
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A;Rosidues: 1-786 cJEL.
A;Groses-references: UNIPROT:P07812; UNIPARC:UPI00001321A4; GB:M32732; GB:J05240; NID:g211;
A;Gronemeyer, H.; Turcotte, B.; Quirin-Stricker, C.; Bocquel, M.T.; Meyer, M.E.; Krozows)
R;Gronemeyer, H.; Turcotte, B.; Quirin-Stricker, C.; Bocquel, M.T.; Meyer, M.E.; Krozows)
R;Gronemeyer, H.; Turcotte, B.; Quirin-Stricker, C.; Bocquel, M.T.; Meyer, A.F.; Meyer, M.E.; Krozows)
A;Title: The chicken progesterone receptor: sequence, expression and functional analysis.
A;Reference number: S06284; MUID:88166640; PMID:3443098
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A;Residues: 1-64, E', 65-786 <CON>
A;Residues: 1-64, E', 65-786 <CON>
A;Residues: 1-64, E', 65-786 <CON>
A;Reference s: UNIPARC:UP10000177C09; GB:M37518

R;Conneely, O.M.; Sullivan, W.P.; Toft, D.O.; Birnbaumer, M.; Cook, R.G.; Maxwell, B.L.; Science 233, 767-770, 1986

A;Title: Molecular cloning of the chicken progesterone receptor.

A;Reference number: A24661; MUID:86289413; PMID:2426779
                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 1-571 a APOH-
A,CTOSS-references: UNIPROT: P36076; UNIPARC:UPI0000052P06; EMBL:Z28088; NID:g486130; PID:
A,Experimental source: strain S288C
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                                                                                                  Cispecies: Saccharomyces cerevisiae
Cibate: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
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                                                                 nypothetical protein YKL088w - yeast (Saccharomyces cerevisiae)
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                                                                                                                                                       C;Accession: 837913
R;Pohl, T.M.; Pohl, F.M.
submitted to the Protein Sequence Database, March 1994
A;Reference number: 837897
A;Accession: 837913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.6%; Score 10; DB 2; Best Local Similarity 100.0%; Pred. No. 0.2; Matches 10; Conservative 0; Mismatches
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A;Map position: 11L
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A; Residues: 1-786 <GRO>
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N;Alternate names: protein F13112.40
N;Alternate names: protein F13112.40
S;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45635
C;Accession: T45635
S;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa submitted to the Protein Sequence Database, November 1999
A;Reference number: Z23010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q57530; UNIPARC:UP100000BEEC9; EMBL:X74123; NID:9510732; PID A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1993 C;Superfamily: T-6b protein
                            A;Residues: 1-1479 <PEO>
A;Cross-references: UNIPROT:Q9Z277; UNIPARC:UPI0000029780; EMBL:AF084480; NID:g4165088;
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R,Drevet, C.; Brasileiro, A.C.M.; Jouanin, L.
Plant Mol. Biol. 25, 83-90, 1994
A,Title: Oncogene arrangement in a shooty strain of Agrobacterium tumefaciens.
A,Reference number: S46509; MUID:94272016; PMID:8003699
A,Accession: S46510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein - Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 26-Dec-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
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A)Status: preliminary
A)Molecule type: DNA
A)Residues: 1-547 <CHO>
A)Cross-references: UNIPROT:Q9SD74; UNIPARC:UPI00000A6868; EMBL:AL133292
A)Experimental source: cultivar Columbia; BAC clone F13112
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1.7%; Score 11; DB 2; Length 1479;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 11; Conservative 0; Mismatches 0; Indels
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1.6%; Score 10; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.19;
iive 0; Mismatches 0; Indels
                                                                                                                                               A;Gene: Wbscr9
A;Map position: 5
F;1360-1415/Domain: bromodomain homology <BRO>
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Best Local Similarity 100.
Matches 10; Conservative
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A; Molecule type: mRNA
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A;Map position: 3
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C, Genetica:

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T45635

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A;Molecule type: DNA
A;Residues: 1-1361 <ODE>
A;Cross-references: UNIPROT:Q04693; UNIPARC:UPI00000530F0; EMBL:Z47816; NID:g642303; PIDN
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R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24492
A;Cross-references: UNIPARC:UP100000694F8; GB:D37935; NID:g1235749; PID:g1235750
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N;Alternate names: hypothetical protein YM9827.03c
C;Species: Saccharomyces cerevisiae
C;Date: 10.Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accesion: S50943
R;Odell, C.; Bowman, S.
submitted to the EMBL Data Library, January 1995
A;Reference number: S50941
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hypothetical protein F17C15.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
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                                                                                                                                         A;Map position: 16L
C;Superfamily: yeast NAB3 protein; ribonucleoprotein repeat homology
C;Keywords: nucleus; RNA binding
F;331-396/Domain: ribonucleoprotein repeat homology <RRM1>
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100.0%; Pred. No. 0.43;
tive 0; Mismatches
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100.0%; Pred. No. 0.35;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                Query Match
1.6%; Score 10; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches
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A,Map position: 13L
                                                C;Genetics:
A;Gene: SGD:NAB3; NAB3; HMD1; MIPS:YPL190c
A;Cross-references: SGD:S0006111
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             382 NEEEEEEED 391
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nes 10; Conserv
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A; Introns: 5/1
A; Note: F17C15.130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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N;Alternate names: probable RNA/ssDNA-binding protein HMD1; protein P1945; protein YPL19
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S48529; 865209; $60122
R;Wilson, S.M.; Oberdorf, A.M.; Datar, K.V.; Swedlow, J.R.; Paddy, M.R.; Swanson, M.S.
submitted to the EMBL Data Library, January 1994
A;Description: Characterization of Nuclear Polyadenylated RNA-Binding Proteins from Saccharomy Discreption number: S48529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPD
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A;Reference number: S65202
                                                   A;Accession: A24312
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kesidues: 417-490 <UE2>
A;Cross-references: UNIPARC:UPI000017139B; GB:M14280; NID:G212607; PIDN:AAA49039.1; PID:
A;Note: amino acid and corresponding nucleotide sequences are also shown for three small
A;Note: amino acid and corresponding nucleotide sequences are also shown for three small
A;Birnbaumer, M.; Hinrichs-Rosello, M.V.; Cook, R.G.; Schrader, W.T.; O'Malley, B.W.
Mol. Endocrinol. 1, 249-259, 1987
A;Title: Chemical and antigenic properties of pure 108,000 molecular weight chick proges
A;Reference number: A40911; MUID:88288199; PMID:3453892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 136-153;168-174;195-228;526-537,'X',539;546-563 <SIM>
A;Cross-references: UNIPARC:UP10000177C0C; UNIPARC:UP10000177C0D; UNIPARC:UP10000177C0B;
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A; Residues: 1-802 <RIE>
A; Residues: 1-802 <RIE>
A; Residues: 1-802 <RIE>
A; Cross-references: UNIPARC: UP1000004F979; EMBL: Z73546; NID: g1370396; PID: g1370397; GSP
A; Cross-references: UNIPARC: UP1000004F979; EMBL: Z73546; NID: g1370396; PID: g1370397; GSP
A; Sugimoto, K.; Matsumoto, K.; Kornberg, R.D.; Reed, S.I.; Wittenberg, C.
Mol. Gen. Genet. 248, 712-718, 1995
A; Title: Dosage suppressors of the dominant G1 cyclin mutant CLN3-2: identification of A; Reference number: $60122; MUID: 96069710; PMID: 7476874
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Rosidues: 128-133, E',138-147, E',149-164;546-558 <BIR>
A;Cross-references: UNIPARC:UPI0000177C0A; UNIPARC:UPI0000177C0B
R;Simpson, R.J.; Grego, B.; Govindan, M.V.; Gronemeyer, H.
Mol. Cell. Endocrinol. 52, 177-184, 1987
A;Title: Peptide sequencing of the chick oviduct progesterone receptor form B.
A;Reference number: A61552; MUID:88005426; PMID:3653503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                 A; Reference number: A24312; MUID:86287271; PMID:2426697
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100.0%; Pred. No. 0.26;
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A;Residues: 1-340,'I',342-802 <SUG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;457-481/Region: zinc finger
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A; Residues: 1-802 <WIL>
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8 셤 4

A; Experimental source: strain Bristol N2; clone C16H3

A; Gene: CESP: C16H3.4 A, Map position: X A, Introns: 26/1 Local Similarity 100.

Best Loc Matches

Query Match

A;Accession: T30045 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-136 <GEI>

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A;Molecule type: DNA
A;Residues: 1-184 <STO>
A;Cross-references: UNIPROT:022801; UNIPARC:UPI00000A10DC; GB:AE002093; NID:92459433; PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S30221
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Nolecule 'type: mRNA
A;Rolecule 'type: mRNA
A;Rolecule 'type: mRNA
A;Residues: 1-186 <ALE>
A;Cross-references: UNIPROT:P26583; UNIPARC:UP1000016AA6C; EMBL:Z17240; NID:g32334; PIDN:A;Note: the nuclectide sequence was submitted to the EMBL Data Library, October 1992
C;Reywords: chromosomal protein
F;1-60/Domain: HMG box homology (fragment) <HMG>
F;69-143/Domain: HMG box homology <HMG1>
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A;Residues: 1-190 <BUR>
A;Residues: 1-190 <BUR>
C;Kross-references: UNIPROT:P05221; UNIPARC:UPI0000171574; GB:Y00204; NID:g64938; PIDN:C?
C;Superfamily: nucleophosmin
C;Keywords: molecular chaperone; nucleus
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R;Burglin, T.R.; Mattaj, I.W.; Newmeyer, D.D.; Zeller, R.; De Robertis, E.M.
Genes Dev. 1, 97-107, 1987
A;Title: Cloning of nucleoplasmin from Xenopus laevis oocytes and analysis of its
A;Reference number: A26630; MUID:88112783; PMID:3428591
A;Accession: A26630
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Spacies: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                       Length 184;
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                                                                                                                                                                                                                                                                                                       1.4%; Score 9; DB 2;
100.0%; Pred. No. 0.74;
tive 0; Mismatches
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1.4%; Score 9; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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A;Status: preliminary
                                                                                                                                                 C,Genetics:
A,Gene: At2g33510
A,Map position: 2
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C;Species: Cricetulus griseus (Chinese hamster)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Gccssion: A27853
R;Lee, K.L.D.; Pentecost, B.T.; D'Anna, J.A.; Tobey, R.A.; Gurley, L.R.; Dixon, G.H.
Nucleic Acids Res. 15, 5051-5068, 1987
A;Title: Characterization of CDNA sequences corresponding to three distinct HMG-1 mRNA A;Reference number: A27853; MUID:87259986; PMID:3601666
A;Rocession: A27853
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R; Geisel, C.; Bradshaw, H. submitted to the RMBL Data Library, August 1996
A; Description: The sequence of C. elegans cosmid C16H3.
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hypothetical protein At2g33510 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: D84746
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
1.4%; Score 9; DB 2; Length 170;
100.0%; Pred. No. 0.69;
tive 0; Mismatches 0; Indels
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Query Match

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RUCIOPOLATE STATE A African clawed frog
C; Cipecies: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C; Accession: A26169
R; Dingwall, C:; Dilworth, S.M.; Black, S.J.; Kearsey, S.E.; Cox, L.S.; Laskey, R.A.
BNBO J. 6, 69-74, 1987
A; Title: Nucleoplasmin cDNA sequence reveals polyglutamic acid tracts and a cluster of B A; Reference number: A26169; MUD: 87218476; PMID: 2884102
A; Residues: 1-200 cDIN>
A; Residues: 1-200 cDIN>
A; Residues: 1-200 cDIN>
A; Cross-references: UNIPROF: PO5221; UNIPARC: UPIO000130A30; GB: X04766; NID: g64939; PIDN: C; Keywords: molecular chaperone; nucleus
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY139008; AAN28956.1; -; mRNA.
InterPro; IPR004827; TF DZIP.
PROSITE; PS00036; BZIP BASIC; UNKNOWN 1.
SEQUENCE 639 AA; 72090 MW; 3A19E0926B9A6406 CRC64;
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Matches 533; Conservative
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181 AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
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10-MAY-2005 (TrEMBLrel. 30, Last seq
10-MAY-2005 (TrEMBLrel. 30, Last ann
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Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brichards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,
N. Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schein J.B., Uones S.J.M., Marra M.A.,
Schnerch A., Schein J.B., Uones S.J.M., Marra M.A.,
Scheerzation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                      Adult retina protein.
Name=LOC153222;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                   TSISSRKRGKRRYFWEYSEQLTPSQQERMLRPSEWNRDTLPSNMYQKNGLHHGKYAVKKS
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Director MGC Project;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC041709, AAH41709.1; -; MRNA.
Ensembl, ENSG00000164463; Homo sapiens.
InterPro; IPR004827; FP bZIP.
PROSITE; PRO0364; BASIP BASIC; UNKNOWN 1.
SEQUENCE 639 AA; 72118 WW; ECFB92D9290DEDEB CRC64;
                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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99.8%; Pred. No. 0;
iive 0; Mismatches 1
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Q8IUR6;
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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S
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                        KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
                                                                                                                                                                                                         301 SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEED
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                                                                                                                                    KINPVOOSRPLLSOIHTDAAKENTCYCGAVAKROEKKGMEPLOGHATPALPFKETQELLL
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The German cDNA Consortium;
Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Boustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Boubmitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, BX647768; CA146039.1; -; mRNA.
Hypothetical protein.
NON TER 408 408
SEQÜENCE 408 AA; 45625 MW; E3E36BFEA8B4284B CRC64;
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Hypothetical protein DKF2p686G2059 (Fragment)
Hymochetical protein DKF2p68G2059 (Fragment)
Hymo sanior
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Hypothetical protein DKFZp313F2319 (Fragment)
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                        Name=DKFZp313F2319
                                                                                                                          NCBI_TaxID=9606
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Li F. Yao K.T.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY174895, AAO18732.1; -; mRNA.
Hypothetical protein.
SEQUENCE 417 AA; 46579 MW; 9DBD37B07C14556B CRC64;
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Best Local Similarity 99.8%; Pred. No. 1.1e-292;
Matches 407; Conservative 0; Mismatches 1;
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QSHYKO;
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241 KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL 300
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinee; Mus.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930001N09 product:hypothetical protein, full insert sequence
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TISSUB=Adipose;
TISSUB=Adipose;
THe German cDNa Consortium;
Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX647573; CAH6104.1; -; mRNA.
InterPro; IPR004827; TF bZIP.
PROSITE; PS00036; BZIP_BASIC; UNKNOWN_1.
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tive 0; Mismatches 2;
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Q9CTQ7;
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                                                           STRAIN=C57BL/6J; TISSUE=Retina;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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NCBI_TaxID=10090;
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Rawai U., Shinagawa A., Shibata K., Yooshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yooshino M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Saito T., Saito T., Saito T., Saito T., Saito T., Saito M., Rabil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ruell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Garibori P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoebbach C., Seya T., Shibata Y., Storch K.-F., Whyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohteuki S., Hayashizaki Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 ALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGLDDFSSPYQDEEVISKTPTLAQL 142
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930040G19 product:hypothetical protein, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 330;
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                             330 AA; 36692 MW; 1397555C4934A64B CRC64;
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Pred. No. 2.8e-76;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                      EMBL; AK020796; BAB32214.1; -; mRNA.
Basembl; BNSWBS00000048249; Mus musculus.
MGI; MGI:1924778; A930001N0981k.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               143 NSEDSOSVSDSLYYPDSLFSVKONPLP 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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clone:4932441F15 product:hypothetical protein, full insert
                          sequence.
Name=A930001N09Rik;
Mus musculus (Mouse)
                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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    library,
  Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Aizawa K., Akimura T., Hara A., Hashizume W., Fukuda S., Furuno M., Hanagaki T., Haraoka T., Hirozane T., Hayathu K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaukwa T., Karoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Karihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Murata M., Ohato N., Okazaki Y., A Saito R., Saitoh H., Sakai K., Sakazume N., Sano H., A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/61; TISSUE-Retina;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                      STRAIN=C57BL/63; TISSUE=Retina; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Ttoh M., Aizawa K., Nagaoka S., Saaski N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Saaski N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishinc H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai U., Rikiki integrated Bequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Mus musculus adult male testis CDNA, RIKEN full-length enriched
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MGI; MGI:1924378; A930001N09Rik.
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08CDG5;
01-MAR-2003 (TEMBLE-1 23,
01-MAR-2003 (TEMBLE-1 23,
01-MAR-2004 (TEMBLE-1 26,
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Matches 87; Conservative
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XX STRAIN=CSTBL/GST TISSUETERETIS;
XX KAWAI O. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
XA Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
XA Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
XA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
XA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
XA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
XA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Xonimi L., M., Staubli F., Suzuki R., Tomita M., Magner L., Washio T.,
XA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Bustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
XA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
XA Anachizaki Y.
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STRANTESTABLÉGI TISSUE-Testis;
The FANTOM COMSOCTIUM.
The RIKEN Genome Exploration Research Group Phase I & II Tesm;
the RIKEN Genome Exploration Research Group Phase I & II Tesm;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                              TRAIN=CSTBL/6G; TISSUE=Testis;

MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

Carninci P., Hayashizaki Y.;

"High-efficiency full-length cDNA cloning.";

Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Testis;
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Best Local Similarity
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SEQUENCE
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Best Local 8
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         SOURCE CONTRACTOR SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURC
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayabhida K., Hayabando K., Hirozane T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsaro N., Okazaki Y., Saitoh K., Saitoh H., Sakai K., Sakazume N., Sakazume N., Sakatoh S., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
"Full-length DDNas from chicken bursal lymphocytes to facilitate
genefunction analysis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.6%; Score 87; DB 2; Length 640; 100.0%; Pred. No. 4.9e-76; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.9%; Score 44; DB 2; Length 131;
100.0%; Pred. No. 2.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 WEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGLDDFSSPYQDEE 131
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                                                                                                                                                                                                                                                                                                                                                                                                            640 AA; 72598 MW; FE02C532FA34E1DE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                      EMBL, AK030092; BAC26779.1; -; mRNA.
Ensembl; ENSMUSG0000048249; Mus musculus.
MGI; MGI:1924378; A930001N09Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 NSEDSQSVSDSLYYPDSLFSVKQNPLP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 NSEDSQSVSDSLYYPDSLFSVKQNPLP 169
                                                                                                                                                                                                                                                                                                                                    Interpro, IPR004827; TF bZIP.
PROSITE, PS00036; BZIP_BASIC; UNKNOWN_1.
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Biol. 6:R6-R6(2005).
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QSZMDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Conservative
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ORFNames=RCJMB04 2h14;
Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Matches
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ID Q4
AC Q4
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Maucell E., Bouneau L., Flacher C., Ozouf-Costaz C., Bernot A., Maucell E., Bouneau L., Flacher C., Ozouf-Costaz C., Bernot A., Nicade S., Jaffe D., Fisher S., Luffalla G., Dossat C., Sequrens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruadu C., Duprat S., Brottier D., Poulain J., De Berardinis V., Rellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., McEwan P., Bosak S., Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Lindbrad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M., Mincker P., Lander E.S., Weissenbach J., Roest Crollius H., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Rajendran K.V., Mukherjee S.C., Vijayan K.K., Jung S.J., Kim Y.J., Oh M.J.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY3744443; AAQ92041.1; -; Genomic_DNA.
                                                                                                                                                                                                            Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FSB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
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13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAF15001, whole genome shotgun sequence.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Wsv286 (Fragment)
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100.0%; Pred. No. 6.6e-24;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 454
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100.0%; Pred. No. 0.093;
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                                                                                                                                                                                  ORFNames=GSTENG00029962001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 431:946-957(2004).
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QGUAY4;
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIM-ATCC 36239 / CBS 767;

Rubmed=15229592; DOI=10.1038/nature02579;

Rubmed=15229592; DOI=10.1038/nature02579;

Bujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,

Boisrame A., Boyer J., Cattolico L., Confanioleri F., Ge Daruvar A.,

Boisrame A., Robre E., Fairhead C., Ferry Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

Reriest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.-M., Nikolski M., Oztaer S., Oztaer-Kalogeropoulos O.,

Boilenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,

Swennen D., Tekais F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,

Mincker P., Soucitet J.-L.,

Mincker P., Soucitet J.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The C. elegans sequencing consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology;" Science 282:2012-2018 (1998).

EMBL; 283239; CABO5181.1; -; Genomic_DNA.

EMBL; 281099; CABO5181.1; -; Genomic_DNA.

EMBL; 283239; CABO5181.1; JOINED; Genomic_DNA.

EMBL; 283239; TABO5811.1; JOINED; Genomic_DNA.

EMBL; Z83239; TABO5811.1; JOINED; Genomic_DNA.

PIN; T23499; T23499.

WormBase; WBGenee00010687; KO8F9.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mortimore B.J.; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468 AA; 53829 MW; F1C367DFC5FE8117 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41_CAEEL
017941_CAEEL PRELIMINARY; PRT; 517 AA.
017941_018079
01-1041-1998 (TrEMBLrel. 05, Created)
01-JAV-1998 (TrEMBLrel. 08, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein K08F9.4.
Caenorhabditis elegans.
                      Saccharomycetales; Saccharomycetaceae; Debaryomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.7%; Score 11; DB 2;
100.0%; Pred. No. 0.23;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                Wincker P., Souciet J.-L.;
"Genome evolution in yeasts.";
Nature 430.35-44(2004).
EMBL, CR382138; CAG89724.1; -; Genomic_DNA.
InterPro; IPR000313; PWWP.
Pfam; PF00855; PWWP; 1.
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PROSITE; PS50812; PWWP; 1.
Complete proteome.
SEQUENCE 468 AA; 53829
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Best Local Similarity 100.
Matches 11; Conservative
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                                          NCBI TaxID=4959;
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QJBS67

QD1-BEC-2001 (TrEMBLrel. 19, Created)

O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypotherical protein.

White spot syndrome virus (WSSV).

Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
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Pred. No. 0.18;
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    Indels
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Shi Z., Bonami J.-R.;
Submitted (GAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF341568; AAL24459.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xia C., Liu J.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB021155; BAA83091.1; -; Genomic_DNA.
SEQUENCE 215 AA; 24441 MW; 913D2D11GBBB7B5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 358 Aa; 40861 MW; FFF05A8A812B2680 CRC64;
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QGBKF1 DEBHA
AC QGBKF1.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 5:milar to CA5208 | IPF2361 Candida albicans IPF2361.
GN OrderedLocusNames-DEHA0F239149;
Obearyomyces hansenii (Yeast) (Torulaspora hansenii).
                                                                                                                                                                                                                                                                                                                           Name=HHNBV-XIA;
unidentified baculovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
VCBI_TaxID=10469;
                                                                                                                                                                                                                                                                                   Last annotation update)
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Q9QTF1;
01-MAY-2000 (TrEMBLrel. 13, C:
01-MAY-2000 (TrEMBLrel. 13, L:
01-OCT-2002 (TrEMBLrel. 22, L:
HHNBV-XIA.
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    11; Conservative
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Gaps

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Length 468; 0; Indels

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WormPep; KO8F9.4; CE11948.
Complete proteome; Hypothetical protein.
SEQUENCE 517 AA; 59610 MW; 68E9E8909D5808FD CRC64;
     S X D
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1.7%; Score 11; DB 2; Length 517;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 11; Conservative 0; Mismatches 0; Indels

380 SENEEEEEEE 390 ||||||||||||||| 21 SENEEEEEEE 31

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Search completed: February 28, 2006, 09:09:46 Job time : 233 secs

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1 MPQPSVSGMDPPFGDAFRSH......GKRRYFWEYSEQLTPSQQER 448
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2005s:*

SUMMARIES

Description	Adk65805 Angiogene	Adq66472 Novel hum	Adk35935 Novel hum	Abp64928 Human pro	_	5 Kapoe	0	٦	1 Kapos	9	4 Kapo	Rat	0 Rat	8 Rat	Ade57830 Rat Prote	Aab85725 Rat TBP-b	Aae37016 Human nuc		Ade56302 Rat Prote	Adp46649 Human col	Adp46648 Human col		Add46092 Human Pro	Aar79912 Human nuc
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ΙD	ADK65805	ADQ66472	ADK35935	ABP64928	ADO20373	AAY96255	AAY58500	AAB62331	ABB05621	ADJ65096	ADV68154	ADE61623	ADD46090	ADE57828	ADE57830	AAB85725	AAE37016	AAW30749	ADE56302	ADP46649	ADP46648	ADE61625	ADD46092	AAR79912
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Score	2364	2148	1268	865	557	190	190	190	190	190	190	185.5	185.5	185.5	185.5	179	169.5	168	168	165	165	165	165	165
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The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present

Aaw84052 Human V3 Aab48964 Human nuc Ad49220 Human nuc Ad458974 Human nuc		Adp.25445 Plasmodiu Abg11270 Novel hum Aay58002 Saccharom Adj58999 Human nuc	Abg04351 Novel hum Adn22802 Bacterial Aae18907 Human PAS Aaw81171 Human BAZ	Abr64241 Angiogene Adp6420 Human PRO Aeb22180 Codon opt Aeb22174 Plasmodiu Abb70151 Drosophil
AAW84052 AAB48964 ADD49220 ADJ58974	ADP54086 ADY19864 ABM80398 ADZ72253	ADP25445 ABG11270 AAY58002 ADJ58999		ABR64241 ADP54420 AEB22180 AEB22174 ABB70151
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## ALIGNMENTS

cytostatic; cardiant; vasotropic; antiarteriosclerotic; angiogenesis inhibitor; angiogenesis stimulator; angiogenic index; gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine. Determining the angiogenic index of a tissue or cell sample using spression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial schemia and/or arteriosclerosis. Anglogenesis-differentially expressed protein ANH0757. Jay G; Claim 23; SEQ ID NO 44; 296pp; English. ADK65805 standard; protein; 639 AA. Fan W, (ORIG-) ORIGENE TECHNOLOGIES INC. 07-FEB-2002; 2002US-00067482. 10-JUN-2002; 2002US-00164595. 16-AUG-2002; 2002US-0403649P. 03-JAN-2003; 2003US-0437746P. 07-FEB-2003; 2003WO-US003848 Li X, Kovacs KF, (first entry) WPI; 2003-731502/69. N-PSDB; ADK65804. WO2003066831-A2. Homo sapiens 06-MAY-2004 14-AUG-2003. ADK65805; Sun Z, ADK65805 ID ADK(  ŝ Ishii

Sato H,

Wakamatsu A,

Sugiyama T,

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 treating cancer,
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invention are useful for diagnosing, preventing and/or treating canc coronary artery disease, myocardial ischemia or coronary arteriosclerosis. They can also be used in research, drug discovery forensic medicine involving angiogenesis. This sequence corresponds one of the differentially expressed proteins of the invention.
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09-MAY-2003; 2003JP-00131392.
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                                                                                                                                   448; Conservative
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Best Local Similarity
Matches 448; Conserv
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The invention relates to 2495 novel polymucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% or 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or moxpid states. They are also useful for tracting osteoprosis, neurological diseases, Alzhaimer's diseases, Parkinson's diseases, dementia and various cancers. This sequence corresponds to a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SLEDCKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPQPSVSGMDPPFCDAFRSHTFSEQTLMSTDLLANSSDPDFMXELDREMNYQQNPRDNFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLPOEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEED
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLEDCKDIENLESFIDVLDNEGALISNWEQWDTYCEDLIKYTKLISCDIWGTKEVDYLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSR
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarthritic; antiparkinsonian; neuroprotective; nootropic; immunosuppressive; cytostatic; antipsoriatic; antinflammatory; antibacterial; antiviral; antifungal; antiparasitic; gene therapy; arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer; psoriasis; inflammatory bowel disease; infection; bacteria; virus; fungus; parasite; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               408
                                                                                                                                                                                                                                                                                                                                                                      Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEDVDDEDHDEGFGSEHELSENEEEEEEEDVEDDKODDISDTFSEPG
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                    90.9%; Score 2148; DB 8;
99.8%; Pred. No. 1.1e-170;
live 0; Mismatches 1;
Otsuki T, Wakam
v Irie R;
                                                                                                                                                 Claim 1; SEQ ID NO 3633; 2449pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADK35935 standard; protein; 256
                        Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                          sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.9 Best Local Similarity 99.8 Matches 407; Conservative
                           Isono Y,
                                                        WPI; 2004-535376/52
                                                                                                                                                                                                                                                                                                                                          Sequence 417 AA;
                                                                        N-PSDB; ADQ64284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004
                             Yamamoto J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
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           Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel
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ADK35935
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Homo sapiens

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This invention relates to a novel isolated polymucleotide comprising a nucleotide sequence selected from one of 1680 sequences, a mature protein coding portion of them, an active domain of them and thehr complementary sequences. The invention may be useful for the production of compounds with an antiarthritic, antiparkinsonian, neuroprotective, nootropic, antibacterial, antiviral, antiparatic, antiparasitic activity. In addition, the disclosed sequences may be useful for gene therapy. The polypeptides or their antibodies are useful for treating many diseases bench as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer, psoriasis, inflammatory bowel disease and infections caused by bacteria, viruses, fungi or parasites. The present sequence is that of a human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPL 124
                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
                                               1. .256
/label OTHER
/note= "OTHER= All Xaa's in this sequence are unknown
amino acids or the site of a stop codon within the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEREEEEEDYEDDKDDDISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 VKONPLPSSFPCKKITSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.6%; Score 1268; DB 5; Length 256; 98.8%; Pred. No. 2.3e-97; cive 0; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 8017; 504pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      for treating, e.g., Parkinson's, Alzheim
disease, and inflammatory bowel disease.
                               Location/Qualifiers
                                                                                                                                                                                                                  05-MAR-2001; 2001WO-US004941.
                                                                                                                                                                                                                                                07-MAR-2000; 2000US-00519705.
19-MAY-2000; 2000US-00574454.
                                                                                                                                                                                                                                                                                                                                     Liu C, Drmanac RT
                                                                                                                   ведиепсе"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-280918/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TFSEPG
                                               Misc-difference
                                                                                                                                                  WO200216439-A2
                                                                                                                                                                                 28-FEB-2002
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                                                                                                                                                                                                                                                                                                                                    rang YT,
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The present invention relates to novel human coding sequences (ABQ99268-ABQ9608) and proteins (ABP64682-ABP65022). The sequences are useful in therapeutic, diagnostic and research methods. The polymucleotides may be used in the field of molecular biology as hybridisation probes, primers for PCR, for chromosome and game mapping, for the recombinant production of protein, or in generation of anti-sense DNA or RNA. The colymucleotides are useful in diagnostics as expressed sequence tags (SSTS) for identifying expressed genes or Ear physical mapping of the human genome. The proteins may be used as molecular weight markers, or and expand cell population in a toripotential or pluripotential state useful for re-engineering damaged or diseased tissues, transplantation, manufacture of bio-pharmaceuticals or the development of bio-sensors. The polymucleotides and proteins are useful for preventing, treating or ameliorating disorders involving aberrant protein expression or biological activity, e.g. haematopoietic disorders, central/peripheral corrections system diseases, mechanical and traumatic disorders, non-healing wounds, immune deficiencies and disorders, infectious diseases caused by viral, bacterial or fungal infection, autoimmune disorders, allergic tractions and conditions, conduction, autoimmune disorders, allergic reactions and conditions, conduction, autoimmune disorders, allergic tractions and conditions, conduction, autoimmune disorders, allergic
                                                                                                                                                                    Human, expressed sequence tag; EST; haematopoietic disorder; central nervous system disease; viral infection; deriphentions described peripheral nervous system disease; non-healing wound; infectious disease; immune deficiency; immune disorder; bacterial infection; allergy; cancer; fungal infection; autoimmune disorder; coagulation disorder; nootropic; antialinflammatory; immunosuppressive; neuroprotective; cytostatic; haemostatic; virucide; antibacterial; fungicide; immunostimulant; cerebroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polymucleotide sequences of the invention were assembled from ESTs isolated mainly by sequencing by hybridisation, and in some cases, sequences obtained from one or more public databases. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire thy wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.6%; Score 865; DB 5; Length 168; 100.0%; Pred. No. 6.4e-64; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iu C, Zhou P, Asundi V,
Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 588; 394pp; English.
ABP64928 standard; protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-2001; 2001WO-US042950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000; 2000US-00714936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT, Goodrich RW, L
Ren F, Xue AJ, Yang Y,
                                                                                                                                   Human protein SEQ ID 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-590824/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABQ99514
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200259260-A2.
                                                                                        25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-2002.
                                             ABP64928;
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282

222

Gaps ; 64

342

402

RESULT 4 ABP64928

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Gaps

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ö 403

Gaps

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DB 8; Length 296;

Score 557; DB 8; Pred. No. 8.7e-38;

23.6%;

0; Mismatches

9

448

(first entry)

(revised)

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1 NLGEQPTKCSPBEDEEDDEEDVDDEDHDEGFGSEHELSENBEEBEVEEDYEDDKDDISDT
                                                   344 NLGEQPTKCSPEEDEEDVDDEDHDEGFGSEHELSENEEBEEEEEDYEDDKDDDISDT
                                                                                                                                                                                                                                                                                                                                               Tafency-associated nuclear antigen; LANA; gamma-2 herpes virus; Human herpes virus 8; HHV8; rindino virus cist-acting element; RVCAE; Kaposi's sarcoma; primary effusion lymphoma; PEL; human immunodeficiency virus; HIV; multicentric Castleman's disease.
                                                                                                                                                                                                                                                                                                                               Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus;
                                                                                                                        61 FSEPGYENDSVEDLKEVISISSRKRGKRRYFWEYSEQLIPSQOER 105
                                                                                                          404 FSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLTPSQQER
                                                                                                                                                                                                                                                                                                        Kaposi's sarcoma-associated herpesvirus LANA.
                                                                                                                                                                                                            AAY96255 standard; protein; 1162 AA
                           Matches 104; Conservative
              Similarity
                                                                                                                                                                                                                                                                 L2-SEP-2003
                                                                                                                                                                                                                                                                              11-SEP-2000
                                                                                                                                                                                                                                       AAY96255;
Query Match
                 Best Local
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                                                                                                                                                                                              AAY96255
                                                                                                                                                                               RESULT
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                 273
                                                                     333
                                                                                               120
                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis, sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sollerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating diseases of the Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy, polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                    MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                               1 MVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKR
                                                                     274 QEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQXKE
                                                                                                                                                                                                                                                                                                                                      Human; PRO; immune related disorder; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schoenfeld J, Williams PM;
                                                                                                                           334 EHNYSLFVSDNLGEQPTKCSPEEDEEDVDDEDHDEGFGSEH 377
                                                                                                                                           EHNYSLFVSDNLGEOPTKCSPEEDEEDVDDEDHDEGFGSEH 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; SEQ ID NO 1266; 1731pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chiu H,
                                                                                                                                                                                                                            ADO20373 standard; protein; 296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-2003; 2003WO-US035268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-NOV-2002; 2002US-0425235P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark H,
                                                                                                                                                                                                                                                                                                           Human PRO polypeptide #633
                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004043361-A2
                                                                                                                                                                                                                                                                                 12-AUG-2004
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WI,
                                                                                                 61
                                                                                                                                                       121
                                                                                                                                                                                                                                                       ADO20373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vovel
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eating or preventing a disease associated with rhodino virus infection a mammal which includes Kaposi's Sarcoma and Primary Effusion
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                                                                   "nuclear localisation signal, NLS'
                                                                                                     "nuclear localisation signal, NLS'
                                                                                                                                                                                              550. .589
/note= "Gln, Glu, Pro, Arg-rich region"
590. .759
                                                                                                                                                                                                                                          /note= "Gln, Glu, Asp-rich region"
760. .840
/note= "Gln, Glu-rich region"
                                                                                                                                                                         /note= "Gln, Glu, Pro-rich region"
                                                                                                                                             "acidic repeat region"
                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaye
                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US027508.
                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00109422.
99US-00298568.
                                                                                                                          .429
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                                                                                        .70
                                                    14. .17
                                                                  /note=
                                                                                                       /note=
                                                                                                                                             /note=
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Human herpesvirus 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-387829/33.
N-PSDB; AAA30290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BALL/) BALLESTAS
(KAYE/) KAYE K M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KIEF/) KIEFF E
                                                                                                                                                                                                                                                                                                                             WO200029626-A1
                                                                                                                                                                                                                                                                                                                                                                                                    19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating or
                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kieff ED,
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Sequence 296 AA;

02-DEC-1999

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theorem is the contracted nuclear antigen (LANA). KSHV is also known as thuman Herpes virus as (HANA) and belongs to the rindino virus, or gamma-2 herpes virus class. The LANA protein is necessary for the efficient persistence of rhadino virus DNA in mammalian cells. Persistent rhadino virus infection is implicated in a variety of diseases e.g. Kaposi's Sarcoma (KS), Primary Effusion Lymphoma (PEL) and multicentric Castleman's disease. In addition, KS is a common malignancy in HIV patients. KSHV persists in host cells in a latent form. One of the few penes expressed from the latent viral DNA is LANA. LANA associates with both human chromosomes and with the rhadino virus cis-acting element (RVCAB), thereby providing a tethering function: the KSHV DNA episome is "tied" to the host chromosomes. This allows the viral DNA to persist in the host call. The present sequence may be used to screen and identify molecules that inhibit LANA interaction with RVCAB, thereby interfering with the latency cycle of this virus. Potential antiviral treatments for the above mentioned diseases may therefore be based on LANA deregulation. (Updated on 12-SEB-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS-------PQ 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 HDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 DDEEDDEEEDEEEDEEEDEEEDEEEDDEDDEDNEDE-----EDDEEEDKKEDEEDGGDGN
                                                                                                                                                                                                                                                                                                                                                                                                                          8.0%; Score 190; DB 3; Length 1162;
24.2%; Pred. No. 3.4e-06;
tive 50; Mismatches 137; Indels 108; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.0%;
Best Local Similarity 24.2%;
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1162 AA;
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10-APR-2000
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buman herpes virus type 8 (HHVB, a gammalherpeavirus). HHVB plays an important role in the pathogenesis of AIDS-related Kaposi's sarcoma. The important role in the pathogenesis of AIDS-related Kaposi's sarcoma. The invention relates to a novel method of detecting the presence of human herpesvirus 8 in a biological sample using peptides representative of dominant antigenic regions of HHVB. The method comprises contacting one or more isolated, immunogenic HHVB peptides with an antibody-containing biological sample, and detecting the formation of a complex beeveen the presence of human herpesvirus 8. The detection of HHVB complex complex between the presence of human herpesvirus 8. The detection of HHVB complex infection can be used to diagnose AIDS-associated Kaposi's sarcoma. The HHVB expectific and the antibodies are useful therapeutically when for the passive immunisation of a human against HHVB infection, thereby reducing HHVB contacted disease. The detection assays are highly specific, sensitive and couract course accurate Early detection and treatment of Kaposi's sarcoma could diminish the severity of symptoms characterisations of Stin disorders. Previous assays for HHVB antibodies such as immunobloces and enzyme immunosassays lack the sensitivity and accuracy needed for reliable diagnosis of Kaposi's sarcoma. Further advantages of municable for repid throughput and screening of samples economically. Cubdated on 06-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                      New methods and compositions for the detection of human herpesvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.0%; Score 190; DB 3; Length 1162;
24.2%; Pred. No. 3.4e-06;
tive 50; Mismatches 137; Indels 108;
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                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 59-62; 68pp; English.
                                                                  99WO-US011407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94; Conservative
                                                                                                                                                                                                                                                       WPI; 2000-097142/08
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                                                                  26-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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434 KTLSIQSSQQQQE-----PQQQEPQQQE 456

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A composition for use in gene therapy comprises an expression vector that includes a nucleic acid sequence encoding a nucleic acid binding protein.
                                                                                                Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis;
Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8;
KSHV; latency-associated nuclear antigen; LANA.
                                                                                 Amino acid sequence of KSHV tethering protein LANA.
                  AAB62331 standard; protein; 1162 AA
                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 9B; 60pp; English
                                                                                                                                                                                                  29-SEP-2000; 2000WO-US026908.
                                                                                                                                                                                                                     99US-00410399.
                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                          Cotter MA;
                                                                                                                                                                                                                                        UNMI ) UNIV MICHIGAN
                                                                                                                                                                                                                                                                            WPI; 2001-281736/29.
N-PSDB; AAF82901.
                                                                                                                                         Human herpesvirus 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1162 AA;
                                                                                                                                                              WO200125484-A2.
                                                                                                                                                                                                                                                          Robertson ES,
                                                                                                                                                                                                                      01-OCT-1999;
                                                      06-AUG-2003
29-JUN-2001
                                                                                                                                                                                 12-APR-2001
                                     AAB62331;
RESULT 8
         AAB62331
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The invention provides a composition comprising nucleic acid, histone H1 protein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone H1 protein, where the rethering protein is LANA. The composition is useful in aiding the retention of the viral DANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histone H1. Methods for screening correction suitable for tethering DNA to Histone H1. Methods for screening of viral proteins the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis, sequence represents the amino acid sequence of the Kaposi,'s sarcoma sequence represents the amino acid sequence of the Kaposi,'s sarcoma antigen (LANA), which acts as a tethering protein. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.0%; Score 190; DB 4; Length 1162;
Best Local Similarity 24.2%; Pred. No. 3.4e-06;
Matches 94; Conservative 50; Mismatches 137; Indels 108; Gaps
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DB 5; Length 1162;

8.0%; Score 190;

Query Match

184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237

SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162

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S09 GPSTLNPICOSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268

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238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285

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The present invention describes a system (A) for maintaining a plasmid as an episome in mammalian cells, comprising the rhadinoviral sequence LANA (latency-associated nuclear antigon) of 3489 base pairs (see ABA93487, 51) expressed in the cell, and the rhadinoviral sequence RVCAE (rhadinoviral cis-acting element) of 801 base pairs (see ABA93488, S2) present in the plasmid Also describes is a method for maintaining a closed circular DNA in a cell by expressing (S1) in the cells and having (S2) as a cis-acting and maintenance sequence in the DNA. (A) is particularly used in gene therapy (or other gene transfer applications) persistence of gene therapy wetcors in cells. The present squence represents Kaposi's sarcoma-associated herpesvirus (KSHV, also called the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the present in the exemplification of the present in the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present in the exemplification of the present expectation of the present exemplification of the p
                                                                                                                                        286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                               269 SSPSEGSWGDDTAMLVLLAEIAERASKNEKECSENNOAGED---NGDNEISKESQVDKDD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            System for episomal retention of plasmids in mammalian cells, useful in gene therapy, comprises rhadinoviral LANA and RVCAE sequences.
                                                                                                                                                                                                                    369 HDEGFGSEHELSENEEEEEEEEDYEDDKDDDISDTFSEPGYENGSVEDLKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaposi's sarcoma-associated herpesvirus; KSHV; LANA; RVCAE; PEL; KSHV terminal repeat; rhadino virus cis acting element; episome; primary effusion lymphoma; latency-associated nuclear antigen; gene therapy; gene transfer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaposi's sarcoma-associated herpesvirus LANA protein.
                                                                                                                                                                                                                                                                                                                              420 -VTSISSRKRGKRRYFWEYSEQLTPSQOE 447
                                                                                                                                                                                                                                                                                                                                                                             434 KTLSIQSSQQQQE-----PQQQEPQQQE 456
                                                                                                               NYSLFVSDNLGEQPTKCSPEEDEEDEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB05621 standard; protein; 1162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaye KM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 7; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-00298568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0109422P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ballestas ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human herpesvirus 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-153769/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1162 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6322792-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2002
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                                                                                                               336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
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The invention relates to an assay for determining whether a compound modulates LANA (latency-associated nuclear antigen) from KSHV (Kaposi's sarcoma-associated nuclear antigen) from KSHV (Kaposi's mediated persistence in a mammalian cell of a DNA episome having RVCAE (rhadinovirus cis-acting element) by detecting whether the compound inhibits expression of a gene resident on that episome. Also included are maintaining a closed circular DNA in a mammalian cell in which LANA is expressed (by using RVCAE as the cis-acting origin and maintenance sequence) and maintaining a plasmid as an episome in a mammalian cell (comprising: (a) Expressing LANA in the cell; and (b) having RVCAE resident on the plasmid). Compounds identified as interfering with the interaction between LANA and RVCAE are useful in treating or preventing thatino virus infection (e.g. primary effusion lymphoma (PEL)). LANA acts in trans on a 0.8 Kb KSHY TR (terminal repeach) unit to mediate efficient

episome persistence. The present sequence represents KSHV LANA

Sequence 1162 AA;

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14;
                                                                                                           163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ 208
                                                                                                                                     238 AKVKINPVQQSRPLL----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
                                                                                                                                                                                                                                                           286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                                                                                                                                                                                                 269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
                                                                                                                                                                                                                                           NYSLFVSDNLGEQPTKCSPEEDEEDEE ---------DVDDED 368
                                                                                                                                                                                                                                                                                            369 HDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE----- 419
                                    124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKONPLPSSFPGKKITSRAAA 183
                                                           111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
                                                                                                                                                              209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268
                                                                                   184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK
            Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHVB; latency-associated nuclear antigen; LANA; primary effusion lymphoma; PEL; virucide; gene therapy; KSHV; Kaposi's sarcoma-associated herpesvirus; episome; RVCAE; rhadinovirus cis-acting element; rhadinovirus infection.
24.2%; Pred. No. 3.4e-06; ive 50; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HHV8 latency-associated nuclear antigen, LANA.
                                                                                                                                                                                                                                                                                                                                                  420 -VTSISSRKRGKRRYFWEYSEQLTPSQQE 447
                                                                                                                                                                                                                                                                                                                                                                    ADJ65096 standard; protein; 1162 AA
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99US-00298568.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-2004 (first entry)
            94; Conservative
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(BALL/) BALLESTAS M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human herpesvirus 8.
 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1998;
21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2004.
                                                                                                                                                                                                                                             336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ65096;
              Matches
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238 AKVKINPVQQSRPLL----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
                                                                                                                                                                                 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                        PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                    ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                                                                111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
                                                                                                                                                                                                                                         336 NYSLFVSDNLGEQPTKCSPREDEEDEE------DVDDED
                                                                                                                                                                                                                                                                                                                               369 HDEGFGSEHELSENEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE-----
8.0%; Score 190; DB 8; Length 1162;
24.2%; Pred. No. 3.4e-06;
tive 50; Mismatches 137; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening; cytostatic; virucide; gene therapy;
latency-associated nuclear antigen; tumor; viral infection;
herpesvirus type 8 infection.
                                                                                                                                   163 PPPSQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaposi's sarcoma-associated herpesvirus LANA protein.
                                                                                                                                                                                                                                                                                                                                                                                     420 -VTSISSRKRGKRRYFWEYSEQLTPSQQE 447
                                                                                                                                                                                                                                                                                                                                                                                                         434 KTLSIQSSQQQQE-----PQQQEPQQQE 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADV68154 standard; protein; 1162 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                             94; Conservative
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-2005
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                               Matches
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ADV68154
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r compounds that modulate rhadino virus LANA action in trans on rhadino virus DNA to mediate efficient episome persistence, detecting whether the compound inhibits expression of a gene

Kaye KM;

Ballestas ME,

Kieff ED,

KAYE K M.

(BALL/) (KAYE/)

WPI; 2004-191011/18.

N-PSDB; ADJ65095

Assays for

a unit of comprises Disclosure; SEQ ID NO 2; 28pp; English.

resident on that episome

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14;
                                                                                                                                                                                                                                                                                 The invention relates to a composition comprising a latency-associated nuclear antigen (LANA) nucleic acid having any of 14 fully defined acquences of 10-61 bp given in the specification (ADV68159-ADV68172). The methods and compositions of the present invention are useful for detecting compounds that are agonistic or antagonistic for the binding of viral genetic material to genomic host DNA, in particular for detecting compounds for treating tumor and viral infections. This sequence corresponds to the LANA protein from the Kaposi's sarcoma-associated herpesvirus (also called human herpesvirus 8). The LANA protein tethers the viral DNA to the human chromosomal structural protein histone H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIXVGSSSDGDTPPRQPPTSPISIGS 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 HDEGFGSEHELSENEEEEEEEDYEDDKDDISDTFSEPGYENDSVEDLKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.0%; Score 190; DB 9; Length 1162;
24.2%; Pred. No. 3.4e-06;
ative 50; Mismatches 137; Indels 108; Gaps
                                                                                                                                                            New composition having a latency-associated nuclear antigen (LANA) nucleic acid, useful for detecting compounds for treating tumors and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447
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                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 2; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 NYSLFVSDNLGEOPTKCSPEEDEEDEE
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                99US-00410399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                  (UNMI ) UNIV MICHIGAN
                                                                                                                       WPI: 2005-038492/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1162 AA;
                                                                                                                                           N-PSDB; ADV68153
                01-OCT-1999;
                                                                                       Robertson ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94;
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the introduction interaction of the nucleic acid sequence. Also derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that increases or decreases the expression of the polymucleotide sequence that is differentially expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a compound that regulates the activity of one or more of the composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaccutical composition comprising the one or more polypucleotides or their antibodies. The polymucleotide or more of modulates its activity is useful for preparing a medicament for treating contains an activity is useful for preparing a medicament for treating contains the polymucleotide or the compound that compare in the component and pharmaccutical composition and pharmaccutical composition and pharmaccutical composition and pharmaccutical composition and pharmaccutical composition comprising the one or more contains and a pharmaccutical composition and pharmaccutical composition and a pharmaccutical composition and a pharmaccutical composition or more of the compound that the compound that the compound that the compound that the compound that the compound that the component and the component and the component and the component and the component and the component and the component and the component and the component and the component and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 DEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKONPLPSSFPGKKITSRAAAPVCSS
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chronic constriction injury; CCI; spared nerve injury; SNI; Chung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 7.8%; Score 185.5; DB 7; Length 712;
1 Similarity 23.3%; Pred. No. 3.9e-06;
84; Conservative 34; Mismatches 134; Indels 109;
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                                                                                                                                          255
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                                                                                                                                                                                                                     The invention discloses a composition comprising two or more isolated rat
                                              ------GFGSEHELSENEEEEEE 389
GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP-----EEDEEDEE 362
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                                                                                                                      EDYEDDKDDDISDTFSE-----PGYENDSVEDLKEVTSISSRKRGKRYFWEYSEQLT
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polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating plan (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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ADE57828
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence witch is differentially regulated in an animal subjected to pain and a skit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more polypeptides or the compound that medicament for treating medicament for the polyment and that may may a method for produced the polymented part for presting a medicament for the presting
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                                                                                                                                            New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
Costigan M;
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Befort K,
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D'urso D,
                                                        WPI; 2003-268312/26
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Sequence 712 AA;

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                                                                                 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS
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7.8%; Score 185.5; DB 7; Length 712; 23.3%; Pred. No. 3.9e-06; vative 34; Mismatches 134; Indels 109; Gaps
                                 Conservative
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The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide a host cell comprising the vector comprising the novel polymucleotide sequence which is differentially regulated in an animal subjected to pain and a compround postform the method, an array, a method for identifying a nucleotide sequence that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal compound that regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a paramaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polymetices its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more polymetices is activity is useful for preparing a medicament for treating pain (c.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed the unit of the printed or the comprised or the comprised or the comparing the note or the painted or the sequence data for this patent did not form directly from WIPO at the paint of the printed or the comparined or the comparined or the comparined or the comparined or the comparined or the comparined or the comparined or the sequence data for this patent end or more therapy.
                                                                                                                                                                                                                       Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.8%; Score 185.5; DB 7; Length 712; 33.3%; Pred. No. 3.9e-06;
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                                                                                                                                                                                   Rat Protein AAA41732, SEQ ID NO 3695.
                                             ADE57830 standard; protein; 712 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page; 1017pp; English
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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84; Conservative 34; Mismatches 134; Indels 109;

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12 ESKKMAPPPKEVEEDSEDEEMSEDEDDSSGEEEVVIPQK-KGKKATTTPAKKVVVS 66	189 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS 248	67 QTKKAAVPTPAKKAAVTPGKKAAATPAKKAVTPAKKVTPA 106	249 RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP 308	107	309 GSLAAGESSSLSASTSVSDSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEE 362	136 GKNAKKEDSDEDEDEEDEDDSDEDEDEFEPPVVKGVKPAKAAPASEDEDEEDDD 195	363 DVDDEDHDE	 DDEEEEEEDDSEEEVMEITPAKGKKTPAKVVPVKAKSVAEEEEDDE	390 EDYEDDKDDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLT 442	256 EDEEDEEDEEDEEBEEEFVKAAPGKRKKEMTKQKEAPEAKKQKIEGSEPTT 308	443 P 443	309 g 309	
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Sequence 44, Application US/10164595

Patent No. 6657054

GENERAL INFORMATION:

APPLICANT: OriGene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
TILE REFERENCE: 1U 103 R1

FILE REFERENCE: 1U 103 R1

CURRENT APPLICATION NUMBER: US/10/164,595

CURRENT FILING DATE: 2002-06-10

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PatentIn version 3.1

SEQ ID NO 44

LENGTH: 639
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US-09-177-431-2
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Query Match

8.0%; Score 190; DB 2; Length 1162;
Best Local Similarity 24.2%; Pred. No. 1.4e-07;
Matches 94; Conservative 50; Mismatches 137; Indels 108;
              369 HDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE
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GENERAL INFORMATION: APPLICANT: ROBERTSON, EILE S. APPLICANT: ROBERTSON, EILE S. APPLICANT: Cotter, Murray A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1162
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8.0%; Score 190; DB 1; Length 1162;
Best Local Similarity 24.2%; Pred. No. 1.4e-07;
Matches 94; Conservative 50; Mismatches 137; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                        APPLICANT: Edelman, Isidore S.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: Immediate Early Protein From Kaposi's
TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA
TITLE OF INVENTION: Encoding Same And Uses Thereof
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/52268/JPW/MSC/SKS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 112-278-0400
TELEPRAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/728,323A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 NYSLFVSDNLGEQPTKCSPEEDEEDEE------
                      TSISSEKKGKKRYFWEYSEQLTPSQQER 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                             Sequence 2, Application US/08728323A
Patent No. 5948676
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Russo, James J.
APPLICANT: Russo, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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Sequence 2, Application US/09298568;
Sequence 2, Application US/09298568;
Patent No. 632792
GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
TITLE OF INVENTION: HIADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF HIADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT PILING DATE: 1999-04-21
EARLIER PILING DATE: 1999-11-19
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PATENTIN USC: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 SSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 ATPALPP--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 SSPSEGSWGDDTAMLVLLAEIAERASKNEKECSENNQAGED---NGDNEISKESQVDKDD 325
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189 KILQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 AKVKINPVQQSRPLL-----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
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                                                                                184 PVCSSKTLQAEVPLSDCVQKASK-----PPSSTQIMVKTNMYHNEKVNFHVECKDYVKK 237
  124 SSPYODEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Glot, Loic
APPLICANT: Manafield, Traci A.
APPLICANT: Manafield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same File REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT APPLICATION NUMBER: 00/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR PLING DATE: 2000-02-01
PRIOR PLING DATE: 2000-02-01
PRIOR PLING DATE: 2000-02-01
SRIGH APPLICATION NUMBER: 60/178,965
PRIOR PLING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 706;
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22.0%; Pred. No. 1e-05;
tive 52; Mismatches 123; Indels
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i OTHER INFORMATION: Polypeptide Accession Number P19338
US-09-538-092-957
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 76; Conserva
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Sequence 2.7 Application US/09894273

GENERAL INFORMATION:
APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: WIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R

CURRENT PAPLICATION NUMBER: US/09/894,273

CURRENT FILING DATE: 1901-60-28

PRIOR FILING DATE: 1998-11-19
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral TITLE OF INVENTION: to Genomic Host DNA FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/09/410,399
CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NO 2
LENGTH: 1162
TYPE: PRI
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                                                                                                                                                                                                                                                                                            Query Match
8.0%; Score 190; DB 2; Length 1162;
Best Local Similarity 24.2%; Pred. No. 1.4e-07;
Matches 94; Conservative 50; Mismatches 137; Indels 108;
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                                                                                                                                                                                                                                ; ORGANISM: Kaposi's sarcoma-associated herpesvirus US-09-410-399-2
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SOFTWARE: PatentIn Ver. 2.0
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TYPE: PRT
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65 CKDIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGLDDFS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 GEQPTKCSPEEDEEDEE------DVDDEDHDEGFGSEHELSENEEEEEED-- 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 SP-----YQDEEVISKTPTLAQLNSEDSQSVS------DSL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QKASKPPSSTQIMVKTNMYHNEKVNFHV-ECKDYVKKAKVKINPVQQ 247
                                                                                                                                                                                                                                                                                                                                                                                     248 SRPLLSQIHTDAAKENTCYC---GAVAKR------QEKKGMEPLQGHATPAL----
                                                                                                                                                                                                                                                                                                                                                               -----NPRDNFLSLED
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                                                                                                                                                                                                                                                                                                                        Indels 215;
                                                                                                                                                                                                                                                                                       Length 709;
FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                             6.8%; Score ...
19.0%; Pred. No. 2.1e-us,
...a 79; Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                             26 TLMSTDLLANSSDPDF-----MYELDREMNYQQ---
TITLE OF INVENTION: FOR DIAGNOSTICS AND THER FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19045
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Patent No. 598987
GENERAL INFORMATION:
APPLICANT: Pillus, Lorraine
APPLICANT: Clarke, Astrid
APPLICANT: Lowell, Joanna
APPLICANT: Jacobson, Sandra
                                                                                                                                                                                                               TYPE: PRT ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 19.0°
Matches 115; Conservative
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Patent No. 6747137
GENERAL INFORMATION:
PAPPLICALIT KEICH WEIBSTOCK et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

WHIGH APPLICATION NUMBER: 60/231,498

WHIGH APPLICATION NUMBER: 60/231,498

WHIGH APPLICATION NUMBER: 60/231,498

WHIGH APPLICATION NUMBER: 60/231,498

WHIGH APPLICATION NUMBER: 60/231,498

WHIGH APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

WUMBER OF SEQ ID NGS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQP-----TKCSPEEDEED 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 EEDVDDEDHDEGFGSEHE-----398
                                                            --LSENEEEEEEEDYEDDKDD 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.0%; Score 165; DB 2; Length 747; 22.0%; Pred. No. 1.1e-05; ive 52; Mismatches 123; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 DISDIFSEPGYENDSVED---LKEVTSISSRKRGKRRYFWEYSEQ 440
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                                                                                                                                                                399 DISDTFSEPGYENDSVED---LKEVTSISSRKRGKRRYFWEYSEQ 440
                                                                                                                                                                                                                                                                   Sequence 10040, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                              361 REDVDDEDHDEGFGSEHE
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Best Local Similarity 22.0%
Matches 76; Conservative
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ORGANISM: Human
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Sequence 21, Application US/09418710
Patent No. 6596482
GENERAL INFORMATION:
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US-09-839-479-21
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20.6%; Pred. No. 3e-05;
tive 62; Mismatches 116; Indels 154; Gaps
           APPLICANT: Reifsnyder, Cheryl
TITLE OF INVENTION: Yeast Silencing Genes, Proteins and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/047,026A FILING DATE: US/09/047,026A FILING DATE: 24-MAR-1998 CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/042,375 FILING DATE: 24-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 831 amino acids
amino acid
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                    ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                             CITY: Boulder
STATE: Colorado
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-047-026A-4
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Matches
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RESULT 10 US-09-418-710-21

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296 HQPNGVIQSVIQEAPLALTIKIKMQSKINENIAAASSTPFSSPVNLSTSGRRTPGNQTPV 355
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177 SVIQSTGLVSNVKPLSLVNQAKKETYMKLIVPSPDVLKAGNKNTSEESSLLTSELRSKRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 160; DB 2; Length 1972;
21.5%; Pred. No. 0.00014;
tive 68; Mismatches 130; Indels 146;
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APPLICANT: JORGES, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042001
CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: DF 9/310027
PRIOR APPLICATION NUMBER: DF 9/310027
PRIOR PILING DATE: 1997-10-19
PRIOR PILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FASELED NOS: 73
SOFTWARE: FASELED FOR WINDOWS VERSION 4.0
SOFTWARE: PASELED FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21, Application US/09839479
Patent No. 6727222
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408 GYENDSVEDLKEVTSISS 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94; Conservative
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CRGANISM: Homo sapiens
US-09-418-710-21
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21;
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                                                                                                                                                                                                                                       67 DIENLESFIDVLDNEGALISNWE------QWDTYCEDLIKYIKLISCDIWGTKEV 115
                                                                                                                                                                                                                                                                                                                                                                     116 DYLGLDDFSSPYQDE--EVISKTPTLAQLNSEDSQSVSDSLYYPDS-LFSVKQNPLPSSF 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 IHNLSISQDSKNKLVTKLAMGNYYKYVDEKLSNNDKQLLQPLRNQKLIIKEEKEKDEEKD
                                                                                                                                       11 PPFGDAFRS--HTFSEQTLMSTDL--LANSSDPDFMYELDREMNYQQNPRDNFLSLEDCK
                                                                                                                                                                  12 PPFHHSTHTHIHTYSYKNTYSSIMTSLHDTTTP-----TTPAPHQHNDSDSDIN-EMSR
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                                                                                                                                                                                                                                                                                                                                                                                                                              173 PGKKITSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMY---HNEKVNFHV
                                              6.7%; Score 157.5; DB 2; Length 738; 20.3%; Pred. No. 5.1e-05;
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21.8%; Pred. No. 0.00025;
tive 68; Mismatches 129; Indels 14
                                                                                             Indels
                                                                                             82; Mismatches 163;
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FULE REFERENCE: 66501-042001
CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR PILLING DATE: 1999-10-15
PRIOR FILLING DATE: 1999-04-17
PRIOR FILLING DATE: 1998-04-17
PRIOR FILLING DATE: 1997-04-18
PRIOR FILLING DATE: 1997-04-18
PRIOR FILLING DATE: 1997-04-18
PRIOR FILLING DATE: 1997-04-18
PRIOR FILLING DATE: 1997-04-18
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FastSEQ for Windows Version 4.0
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                                              Query Match
Best Local Similarity 20.39
Matches 102; Conservative
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Matches 95; Conser
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    US-09-248-796A-16666
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Requence 16666, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
THERE PREFERENCE: 107196-61.32
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 16666
LENGTH: 738
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LOCATION: (154)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 ---SPEEDEEDEEDVODEDHDEGFGSEHELSENEEEEEE--EEDYEDDKODDISDTFSEP 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 SRAAAPVCSSKTLQAEVPL----SDCVQKASKPPS--STQI--MVKTNMYHNEKVNFH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SQKKEEHNYSLFVSDNLG-----EQPTKC-----SQKKEEHNYSLFVSDNLG----
                                                                                                                                                                                                                                                                                      Query Match 6.8%; Score 160; DB 2; Length 1972; Best Local Similarity 21.5%; Pred. No. 0.00014; Matches 94; Conservative 68; Mismatches 130; Indels 146; Gaps
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-100-24
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 GYENDSVEDLKEVTSISS 425
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ORGANISM: Candida albicans
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US-09-839-479-21
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                                                                                                                                                                     LENGTH: 1972
TYPE: PRT
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296 HQPNGVIQSVIQEAPLALTIKIKMQSKINENIAAASSTPPSSPVNLSTSGRRIPGNQTPV 355
                                                                                                                                                                                                                                                                                      411 SNEDEREDDEREDEREDDESDDSQSESDSNSESDTEGSEREDDDXXQQDESDSTEG-- 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 687;
                                                                                   302 PLP-----QEGP-----GSDAGESSSLSASTSVSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.6%; Score 155.5; DB 2; Length (Best Local Similarity 25.8%; Pred. No. 6.8e-05; Matches 51; Conservative 34; Mismatches 70; Indels
261 KENTCYCGAVAKRQEKKGME-----PLQGHATPALPFKETQE-
                                                                                                                                                                           329 -----SQKKEEHNYSLFVSDNLG-----EQPTKC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2651, Application US/10104047
Sequence 2651, Application US/10104047
Patent No. 6943241.
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: 2002-03-25
CURRENT FILING DATE:
PRIOR FILING DATE:
NUMBER OF SEQ 1D NOS: 4096
SOSTWARE: Patentin Ver. 2.1
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256 KRKKEMAKQKAAPEAKKQ 273
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469 EKTSMK-LNKTTSSKS 483
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US-10-104-047-2651
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US-10-104-047-2651
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                                                                     ------VECKDYVKKAK----VKI------NPVQQSRPLLSQIHTDAA 260
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63 GISSSDSDDLEEDEEEEEDQSIEESEDDDSDSESEAQHKSNNQVLLHGISDPKA-DGQKAT 121
                                            179 SRAAAPVCSSKTLQAEVPL----SDCVQKASKPPS--STQI--MVKTNMYHNEKVNFH-
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Best Local Similarity 21.8%; Pred. No. 0.00025;
Matches 95; Conservative 68; Mismatches 129; Indels 144; Gaps
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6727222
GENERAL INFORMATION:
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Sequence 2651, Applisequence 1332, Applisequence 1332, Applisequence 12480, Applisequence 1280, Applisequence 2031, Applisequence 313, Applisequence 3126, Applisequence 1513, Applisequence 1513, Applisequence 1513, Applisequence 1513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Applisequence 23513, Appli

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Publication No. US20050106579A1

GENERAL INFORMATION:

APPLICANT: Original Section of TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides

FILE REFRENCE: 1U 103 R1

CURRENT APPLICATION NUMBER: US/10/717,665

CURRENT FILING DATE: 2003-11-21

PRIOR APPLICATION NUMBER: US/10/164,595

PRIOR PLIANG DATE: 2002-06-10

NUMBER OF SEC 1D NOS: 80

SOFTWARE: Patentin version 3.1

SEQ ID NO 44
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100.0%; Pred. No. 9.4e-153;
tive 0; Mismatches 0;
US-10-104-047-2651

US-11-013-684-7

US-10-408-7654-1332

US-10-408-7654-1332

US-10-408-7654-1280

US-10-408-7654-1280

US-10-450-763-1280

US-10-450-763-46978

US-11-097-143-30126

US-10-978-242-3

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Matches 448; Conservative
        TYPE: PRT
ORGANISM: Homo sapiens
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   420
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Publication No. US20040037847A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Ballestas, Mary E.
APPLICANT: Raye, Kenneth M.
TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE FILE REFERENCE: 16412-10001R
CURRENT PALICATION NUMBER: US/09/894,273
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/109,422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 PPPSQQTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ
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   361 EEDVODEDHDEGFGSEHELSENEEEEEEDYEDDKODDISDTFSEPGYENDSVEDLKEV
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                                                                                                                                   US-10-732-923-3319

US-10-732-923-3319

Sequence 3319, Application US/10732923

Publication No. US20050108791A1

GENERAL INFORMATION:

TILE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

TILE REPERENCE: 38-15 (52796) C

CURRENT APPLICATION NUMBER: US/10/732,923

CURRENT FILING DATE: 2003-12-10

PRIOR FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 24149

SEQ ID NO 3319
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8.1%; Score 191.5; DB 5;
Best Local Similarity 24.7%; Pred. No. 0.00028;
Matches 92; Conservative 53; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT ; ORGANISM: Kaposi's sarcoma-associated herpesvirus 198-10-732-933-3319
                                                            TSISSRKRGKRRYFWEYSEQLTPSQQER
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US-09-894-273-2
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111 SSPIPPSHPVSPGTT-----DTHSPSPALPPTQSPESSQRPPL-SSPTGRPDSSTPMR 162
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APPLICANT: Robertson, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA TITLE OF INVENTION: to Genomic Host DNA FILE REFERENCE: UM-03778
CURRENT APPLICATION NUMBER: US/10/294,804
CURRENT PILING DATE: 2002-11-14
PRIOR FILING DATE: 1999-10-01
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8.0%; Score 190; DB 4; Length 1162;
Best Local Similarity 24.2%; Pred. No. 0.00043;
Matches 94; Conservative 50; Mismatches 137; Indels 108;
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
                                                                                                                                                                                                                          8.0%; Score 190; DB 3; I
24.2%; Pred. No. 0.00043;
trive 50; Mismatches 137;
                                                                                                                                         ORGANISM: Kaposi's sarcoma-associated herpesvirus
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SOFTWARE: PatentIn Ver. 2.0
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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Matches 94; Conserv
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293 KETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNY-----SLFVSDNL 345
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                                                                                                                                                                                                                                                        RICHARDSON, Thomas W.; WARREN, Bridget A.;
GRIFFIN, Jennifer A.; TANG, Y. TOM;
YUE, Henry BAUGHN, Mariah R.;
EMBKLING, Brooke M.; LAL, Preeti G.;
LU, Dyung Aina M.; FORSYTHE, Ian J.;
RAMKUMAR, Jayalaxmi; LI, Joana X.;
BCHA, Shanya D.; DUGGAN, Brendan M.;
SANJANWALA, Madhusudan M.; LEE, Ernestine A.;
BURFORD, Nail; ELLIOTT, Vicki S.;
ISON, Craig H.; DING, Li,
BOROWSYY, Mark L.; YAO, Monique G.;
BARROSO, Ines; TRAN, Bao;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WALIA, Narinder K.; HAFALIA, April J. A.; APPLICANT: NGUYEN, Danniel B.; LU, Yan; APPLICANT: ARVIZU, Chandra S. TITLE OF INVALION: NUCLEIC ACID-ASSOCIATED PROTEINS FILE REPERENCE: PF-1068 USN CURRENT APPLICATION NUMBER: US/10/483,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%; Score 169.5; DB 5;
24.5%; Pred. No. 0.006;
tive 44; Mismatches 120;
                                                                                                                                                                                                                           INCYTE CORPORATION; SWARNAKAR, Anita;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7037554CD1
US-10-483-505-3
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PRIOR APPLICATION NUMBER: PCT/US02/21971
PRIOR PILING DATE: 2002-0-10
PRIOR PILING DATE: 2002-0-10
PRIOR PELICATION NUMBER: US 60/305,089
PRIOR PILING DATE: 2001-07-12
PRIOR PELICATION NUMBER: US 60/305,104
PRIOR PILING DATE: 2001-07-12
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
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PRIOR PILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 2001-07-20
PRIOR PILING DATE: 2001-07-20
PRIOR PILING DATE: 2001-07-20
PRIOR PILING DATE: 2001-07-27
PRIOR PILING DATE: 2001-07-27
PRIOR PILING DATE: 2001-07-27
PRIOR PILING DATE: 2001-07-27
                                                                                                     Sequence 3, Application US/10483505 Publication No. US20050118582A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 86; Conserva
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208
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                                                                     209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS 268
                                                                                                                                                                                                                                                                                                                                                                          286 ATPALPF--KETQELLL-----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH 335
                                                                                                                                                                                                                                   269 SSPSEGSWGDDTAMLVLLAEIAEEASKONEKECSENNQAGED---NGDNEISKESQVDKDD 325
                                                                                                                                                                                                                                                                                                                     ----- 368
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----SQIHTDAAKENTCYCGAVAKRQEKKGMEPLQ----GH 285
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; Pred. No. 0.00043;
50; Mismatches 137; Indels 108;
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TITLE OF INVENTION: LANA Viral Protein Binding Sites
FILE REPERENCE: UM-07142
CURRENT APPLICATION NUMBER: US/10/194,046
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: 09/410,399
PRIOR FILING DATE: 1999-10-01
SUMMER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
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ORGANISM: Kaposi's sarcoma-associated herpesvirus
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                                                                                                                                                                                                                                                                                                                 336 NYSLFVSDNLGEQPTKCSPEEDEEDEE----
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Publication No. US20040248081A1
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Best Local Similarity 24.2%;
Matches 94; Conservative 50
        238 AKVKINPVQQSRPLL--
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APPLICANT: HOVANGESIAN, ARA
APPLICANT: Callebaut, Christian
APPLICANT: Callebaut, Christian
APPLICANT: Callebaut, Christian
APPLICANT: Waller, Sylviane
APPLICANT: Briand, Jean-Paul
APPLICANT: Briand, Jean-Paul
APPLICANT: Guichard, Galles
TITLE OF INVENTION: A NOVEL CELL SURFACE RECEPTOR FOR HIV RETROVIRUSES,
TITLE OF INVENTION: A NOVEL CELL SURFACE RECEPTOR FOR HIV RETROVIRUSES,
TITLE OF INVENTION: A NOVEL CELL SURFACE RECEPTOR FOR HIV RETROVIRUSES,
TITLE OF INVENTION: A NOVEL CELL SURFACE RECEPTOR FOR HIV RETROVIRUSES,
TITLE REFERENCE: 03495.0166-01000
CURRENT FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 907-933,302
PRIOR APPLICATION NUMBER: 607-09-10
PRIOR APPLICATION NUMBER: 607-09-10
PRIOR PELING DATE: 1999-03-12
PRIOR PELING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 32
SOFTHARE: PATENTIN OF: 2.1
SEQ ID NO 22
LENGTH: 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQP-----TKCSPEEDEED 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------ 398
346 G-----EQPTKCSPEEDEEDEEDVD----DEDHDEGFGSEHELSENEEEEEEEEDYED 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 KN---GKNAKKEDSDEEEDDDSEEDEEDDEDEDEDEDEIEPAAMKAAAAAPASEDEDDED 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSS
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                                                                                                                                              395 DKDD------DISDTFSEP-GYENDSVEDLKEVTSISSRKRGKRR 432
                                                                                                                                                                     399 DISDTFSEPGYENDSVED---LKEVTSISSRKRGKRRYFWEYSEQ 440
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                                                                                                                                                                                                                                                                                          Sequence 22, Application US/09825886 Publication No. US20020076693A1 GENERAL INFORMATION:
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US-09-825-886-22
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RESULT 8

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APPLICANT: BRIAND, JEAN-PAUL
TITLE OF INVENTION: INHIBITION OF VIRUS ANCHORAGE BY RGG DOWAIN OF A CELL SURFACE-
TITLE OF INVENTION: INHIBITION POLYNUCLEOTIDE CODING FOR SAID RGG DOWAIN,
TITLE OF INVENTION: EXPRESSED PROTEIN, POLYNUCLEOTIDE CODING FOR SAID RGG DOWAIN,
TITLE OF INVENTION: PROTEIN LIGAND BINDING TO THE CELL-SURFACE-EXPRESSED PROTEIN
FILLE REFERENCE: 03495.0260-00000
CURRENT APPLICATION NUMBER: US/10/384,569
CURRENT APPLICATION NUMBER: 60/393,371
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/397,600
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VEY: 2.1
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APPLICANT: Rouslahti, Erkki
APPLICANT: Rouslahti, Erkki
APPLICANT: Porkka, Kimmo
APPLICANT: Christian, Sven
TITLE OF INVENTION: HARDS Peptides and Related Molecules
TITLE OF INVENTION: HARDS Peptides and Related Molecules
TITLE OF INVENTION: HARDS PEPTICATION WINBER: US/10/400,083
CURRENT APPLICATION NUMBER: US/10/400,083
CURRENT FILING DATE: 2003-03-03-20
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 20
SUFTWARE: PRASTSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 EEDVDDEDHDEGFGSEHE-----
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Sequence 3, Application US/10384569 Publication No. US20040002457A1 GENERAL INFORMATION:
                                                                                                APPLICANT: HOVANESSIAN, ARA G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: DOMAIN
LOCATION: (117)...(167)
LOCATION: (117)...(167)
COTHER INFORMATION: Neuromodulin (GAP-43) proteins domain identified by eMATRIX,
COTHER INFORMATION: accession number BL00412D, p-value=8.644e-15, raw score of 16.54
US-10-450-763-41629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 SQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEEEEEE 308
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                                                                                                                                                                                                                                                   361 EEDVDDEDHDEGFGSEHE-----398
                                                                                                                                                                                                                                                                          -----AVTTPGKKGATP--GKALVATPGKKG-----AAIPAKGA 134
---KAAATPAKKTVTPAK-- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 PGDRHAPPLAPSGLSPEL---TLPQTQCCAQATVQGLEGTRSWSQSGTSSLSPWSHTSLR
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                                                 249 RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP
                                                                                                                                                 309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQP-----TKCSPEEDEED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | Sequence 41629, Application US/10450763
| Sequence 41629, Application US/10450763
| Publication No. US20050196754A1
| CENERAL INFORMATION:
| APPLICANT: Hyseq, Inc
| TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
| FILE REPERENCE: 790C1P3/US
| CURRENT APPLICATION NUMBER: US/10/450,763
| CURRENT FILING DATE: 2003-06-11
| PRIOR APPLICATION NUMBER: 09/540,217
| PRIOR PILING DATE: 2000-03-30
| PRIOR PILING DATE: 2000-03-31
| PRIOR PILING DATE: 2000-03-31
| PRIOR PILING DATE: 2000-08-23
| NUMBER OF SEQ ID NOS: 60736
| SEQ ID NO 41629
| LENGTH: 167
                                                                                                                                                                                                                                                                                                                                                      399 DISDTFSEPGYENDSVED---LKEVTSISSRKRGKRRYFWEYSEQ 440
                                                                                                                                                                                                                                                                                                                                                                                                    252 DDEDDDDEDDEEEEEEEEEPVKEAPGKRKKEMAKOKAAPEAKKO 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.9%; Score 162; DB 5; Length 16 Best Local Similarity 30.5%; Pred. No. 0.0029; Matches 46; Conservative 28; Mismatches 55; Indels
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) Publication No. US20050196754A1
) GENERAL INFORMATION:
A PAPLICANT: Hyseq, Inc
TITLE OF INVENTION:
PILE REFERENCE: 790CIP3/US
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     68 PT--KKVAVATPAKKAAVTPGK-
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                        PT--KKVAVATPAKKAAVTPGK-----102
                                                                                                                                                                                                                                                                                                                                                                                                            249 RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQP-----TKCSPEEDEED 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --LSENEEEEEEEDYEDDKDD 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AVTTPGKKGATP--GKALVATPGKKG-----AAIPAKGA 134
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                                                                                                                                                        Gaps
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CURRENT APPLICATION UNMBER: US/10/491,545A
CURRENT FILING DATE: 2004-04-01
PRIOR APPLICATION NUMBER: US 60/327,212
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US 0/327,212
PRIOR APPLICATION NUMBER: US 0/327,212
PRIOR APPLICATION DATE: 2001-10-03
PRIOR FILING DATE: 2002-10-02
                                                                                                            7.0%; Score 165; DB 4; Length 707;
22.0%; Pred. No. 0.012;
tive 52; Mismatches 123; Indels 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 DDEDDDEDDEEEEEEEEPVKEAPGKRKKEMAKQKAAPEAKKQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 DISDIFSEPGYENDSVED---LKEVISISSRKRGKRRYFWEYSEQ 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao, Haoran
Rigel Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/10491545A Publication No. US20050130117A1 GENERAL INFORMATION:
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APPLICANT: Li, Congfen
APPLICANT: Liao, X. Charlene
APPLICANT: Masuda, Esteban
                                                                                  Query Match
Best Local Similarity 22....
Best Local Schilarity 22....
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pardo, Jorge
                                    ORGANISM: Homo sapiens
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                                                              US-10-400-083-19
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APPLICANT:
APPLICANT:
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1436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1767 DEMDEEEDDDSFGND-----EFFEDEEETPEDDDDDDVVVLSDGDDEPANDNDB-ESLN 1819
                                                                                                                                                                                                                                                                                                                                                                                                                                 1535 PVPSDNIPDPTRPPTNSPGTVLPVPHTPQTSVRVPTQSLFSSSSTTTVQPQPEKKKVVLPSI 1594
                                                                                                                                                                                                                                                                                                           54 NPRDNFLSLEDCKDIENLE-----SFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTS 106
                                                                                                                                                                                                                                                                                                                                                                                                      107 CDIWGTKEVDYLGLDDFSSPYQDEEVISKTPT--LAQLNSEDSQSVSDSLYYPDSLFSVK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 HTDAAKENTCYCGAVAKRQEKKGMEPLQ-----GHATPALPFKETQELLLSPLPQEGPG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 ONPLPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCVQKASK----PPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 ---STQI---MVKTNMY-----HNEKVNFHVECKD-YVKKAKVKINPVQQSRPLLSQI
                                                                                                                                                                                                                6.8%; Score 160.5; DB 4; Length 1974; 21.6%; Pred. No. 0.088;
                                                                                                                                                                                                                                                                                                                                           51; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09839479
Publication No. US20020039779A1
GENERAL INFORMATION:
APPLICANT: JONES, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REPRENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
CURRENT FILING DATE: 2001-04-20
FRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-0-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 NLGEOPTKC----SPEEDEED----
       60/360,039
                                                                                                                        TYPE: PRT
ORGANISM: Caenorhabditis elegans
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 SLAAGESSSLSAS----
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LENGTH: 1972
                                                                            SEQ 1D NO 5455
                                                                                                  LENGTH: 1974
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NAME/KEY: DOMAIN
LOCATION: (308)...(343)
OTHER INFORMATION: Matrix protein (MA) p15. domain identified by eMATRIX,
OTHER INFORMATION: accession number PF01140D, p-value=2.570e-09, raw score of 15.54
US-10-450-763-34710
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APPLICANT: Gain, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Xianten
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION UNMBER: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 ENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 STDLLANSSDPDFMYELDREMNYQQNPRDNFLSLEDCKDIENL--ESFTDVLDNEGALTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 NWEQWDTYCEDLTKYTK----LTSCDIWGTKEVDYLGLDDFSSPYQDEEVISKTPTLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 LNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCV
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Best Local Similarity 20.2%; Pred. No. 0.011;
Matches 86; Conservative 58; Mismatches 125; Indels 157; Gaps
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                      CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/USO1/08631
PRIOR PILING DATE: 2000-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PILING DATE: 2000-08-23
NUMBER: OF SEQ ID NOS: 60736
CURRENT APPLICATION NUMBER: US/10/450,763 CURRENT FILING DATE: 2003-06-11
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US-10-369-493-5455
'S equence 5455, Application US/10369493
'Publication No. US20030233675A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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LENGTH: 382
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                                                                                                                                  179 SRAAAPVCSSKTLQAEVPL----SDCVQKASKPPS--STQI--MVKTNMYHNEKVNFH- 228
                                                                                                                                                                                         ------VECKDYVKKAK----VKI-----NPVQQSRPLLSQIHTDAA 260
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                                             Query Match 6.8%; Score 160; DB 3; Length 1972;
Best Local Similarity 21.5%; Pred. No. 0.095;
Matches 94; Conservative 68; Mismatches 130; Indels 146; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.8%; Score 160; DB 4; Length 1972; Best Local Similarity 21.5%; Pred. No. 0.095; Matches 94; Conservative 68; Mismatches 130; Indels 146;
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FILE REFERENCE: 06501-042001
FURENT APPLICATION NUMBER: US/09/418,710
FRIOR APPLICATION NUMBER: US/09/418,710
FRIOR RILING DATE: 1999-10-15
FRIOR PILING DATE: 1999-10-15
FRIOR PILING DATE: 1999-10-15
FRIOR PILING DATE: 1997-10-24
FRIOR FILING DATE: 1997-04-17
FRIOR PILING DATE: 1997-04-17
FRIOR FILING DATE: 1997-04-18
FRIOR RELIGATION NUMBER: UP 9/116570
FRIOR PILICATION NUMBER: UP 9/116570
FRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 73
SOFTWARE: FABELSEQ FOR WINDOWS VERSION 4.0
LENGTH: 1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 21, Application US/10376537; Publication No. US20030224405A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-839-479-21
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411 SNEDEEEDDEEDEEDDEED-DESDDSQSESDSNSESDTEGSEEEDDDKDQDESDSDTEG 469
228
                                                                                                   -----VECKDYVKKAK----VKI-----NPVQQSRPLLSQIHTDAA 260
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179 SRAAAPVCSSKTLQAEVPL----SDCVQKASKPPS--STQI--MVKTNMYHNEKVNFH-
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470 --EKTSMKLNKTTSSVKS 485
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38, Appl 14, Appl 2, Appl 1413, Ap 351, Ap 200, App 2037, A 4, Appl 8, Appl 8, Appl 4, Appl 4, Appl 4, Appl 5, Appl 5, Appl 5, Appl 5, Appl 5, Appl 5, Appl

Sequence:

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Searched:

Database

Result 8 

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APPLICANT: INSTITUT PASTEUR
APPLICANT: INSTITUT PASTEUR
APPLICANT: INSTITUT PASTEUR
APPLICANT: INSTITUT PREBRE
TITLE OF INVENTION: IDENTIFICATION OF A CONSERVED REGION OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: MSP3 TARGETED BY BIOLOGICALLY ACTIVE ANTIBODIES
FILE REPERENCE: 275601US0
CURRENT PAPPLICATION NUMBER: US/11/189,817
PRIOR FILING DATE: 2005-07-27
PRIOR FILING DATE: 2004-08-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATCHIN VERSION 3.3
SOFTWARE: PATCHIN VERSION 3.3
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I Similarity 20.9%; Pred. No. 0.00034;
82; Conservative 61; Mismatches 146; Indels 104; Gaps
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169 KAKNAYQKAN------
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3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO3_NEW_PUB.pep:*

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Copyright (c) 1993 - 2006 Biocceleration Ltd
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APPLICANT: Hongin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CLO01519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR APPLICATION NUMBER: US 60/568,609
PRIOR APPLICATION NUMBER: US 60/569,554
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-25
PRIOR PILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
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TITLE OF INVENTION: Novel full length CDNA
FILE REFERENCE: 084335-0191
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CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
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ISHII, SHIZUKO
YAWAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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SOFTWARE: Patentin Ver. 2.1
EQ ID NO 2651
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IRIE, RYOTARO
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Publication No. US20060024324A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Vaccines comprising chimeric malaria proteins derived from Plasmor TITLE OF INVENTION:
FILE REPRENCE: 150074k

TITLE OF INVENTION:
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----BEEAEETEEBELEEKNEEE---TESEISEDEEEEEEEEKEEENDKKKEQEKEQSN 289
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                                                                                                                                                                        409 YENDSVEDLKEVTSISSRKRGKRRYFWEYSEQL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 PQEGPGSLAAGESSSLSASTSV-SDSSQ-----
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8 엄 ò 요 ò 요 8 유 ò Sequence 2651, Application US/11072512 Publication No. US20060029945A1 GENERAL INFORMATION: APPLICANT: ISOGAL, TAKAO

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391 RIDEVISKYAMLQDKSEBGERKKRRARLQGTSSHS---ADTPEASLD--SGEGPSGMASQ 445
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                                                                                                                                                                                                                                                                                       314 GESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGF 373
                                                                                                                                                                                                                                                                                                                              446 GCPSASRAETDDEDDBESDEEEE-------EBEBEBEBEBEBEADSBEBEDD. 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 GSEHELSENBEBEBEBEDYEDDKODDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRR 432
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                     210 STQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKEN-----
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APPLICANT: Meses et al.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
TITLE REFERENCE: 21402-240CIP
CURRENT APPLICATION NUMBER: 06/261,014
PRIOR APPLICATION NUMBER: 60/261,014
PRIOR APPLICATION NUMBER: 60/261,018
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR FILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/261,026
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR APPLICATION NUMBER: 60/261,029
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR APPLICATION NUMBER: 10/044,564
PRIOR FILING DATE: 2001-09-17
PRIOR FILING DATE: 2001-09-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.1
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; Pred. No. 0.042;
40; Mismatches
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US-11-054-281-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TCYCGAVAKROE---KKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAA- 313
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TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof;
FILE REFERENCE: CLOOIS19.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
CURRENT PILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR PILING DATE: 2004-05-07
PRIOR PILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-06-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 760
                                                                                                                                                                                                                                                                                                                                                                     113 KEVDYLGLDDFSSPYQDE----EVISKTPTLAQLNSEDSQSVSDSLY-----YP
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                                                                                                                                                                                                                           6.4%; Score 150.5; DB 7; Length 740; 23.1%; Pred. No. 0.0058;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                      55; Mismatches 142;
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 292, Application US/11124367A Publication No. US20060024700A1 GENERAL INPORMATION:
APPLICANT: Michele Cargill APPLICANT: Hongjin Huang
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.14
Matches 83; Conservative
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                                                                                                                                          sapiens
                                                                                                                                   ORGANISM: Homo
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                            SEQ ID NO 293
LENGTH: 740
TYPE: PRT
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US-11-054-281-108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            703 HSSINQENGTANPIKNGK-----TSP-----ASKDQRTGKKTSVQGQVQKGNDE 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              582 LPAQVGTIMDSSYSANRQVFFQSVADKEAİANFTNQKNISNPPDMSG------WNPFG 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDLTKYTKLTSCDIWGTKEVDYLGLDDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLY 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 POPSASOYPTWMPQYQQAF----FQQOMLAQHQPSQQQASPEYLTSPOEFSPALVSYTSS 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1254, Application US/10821234
Publication No. US20050255114A1
GRNERAL INFORMATION:
APPLICANT: Labar, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 KTNMYHNEKVNFHVECKDYVKKAKVKINPVOOSRPLLSQIHTDAAKENTCYCGAVAKROE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.9%; Score 140; DB 6; Length 1168; Best Local Similarity 19.3%; Pred. No. 0.05; Matches 90; Conservative 55; Mismatches 136; Indels 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  387 EEEE-----DYEDDKD--DDISDTFSEPGYENDSVEDLKEVTSISSR 426
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                                                                    JUNERAL ALCALING. Simon

TITLE OF INVENTION: Human BMP2 Inducible Kinases
FILE REFERENCE: 004974.01015
FILE REFERENCE: 004974.01015
CURRENT PELLING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: US/10/509,422
CURRENT FILING DATE: 2003-03-20
PRIOR PILING DATE: 2003-03-20
PRIOR FILING DATE: 2003-03-27
PRIOR FILING DATE: 2002-03-27
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
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PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
PRIOR FILING DATE: 2002-08-30
          Sequence 2, Application US/10509422
Publication No. US20050244825A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-821-234-1254
                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1168
TYPE: PRT
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US-10-509-422-2
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                                                                                                                                                                                                                                                                                                                                                                                   ----LSENEEEEEE 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 PILAMPGRNKAK-STCSCPDL----OPNGODLGENSRVARLGADESEE-----EGRR 92
                                                                                                                                                                                                                                                                                                                                                                                                                 364 VDDEDHDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKE 419
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                   25;
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CURRENT PILING DATE: 2005-02-08

PRIOR FILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR PILING DATE: 2001-01-11

PRIOR APPLICATION NUMBER: 60/261,018

PRIOR PILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-01-11

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PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-01-11

PRIOR FILING DATE: 2001-08-17

PRIOR FILING DATE: 2001-08-17

PRIOR FILING DATE: 2001-08-17

PRIOR FILING DATE: 2002-01-11
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                                                                                                                                                                                                                                                                                Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 DYEDDKODDISDTFSEPGYENDSVED---LKEVTSISSRKRGKRR 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                              Query Match
5.9%; Score 138.5; DB 6
Best Local Similarity 30.5%; Pred. No. 0.0053;
Matches 32; Conservative 20; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 0.05
35; Mismatches
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: Dt_SEQ_Genes Version 1.0
SEQ ID NO 1254
                                                                                                                                                                                                                                                                                                                                                                                      353 SPEEDEEDEEDVDDEDHDEGFGSEHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 108, Application US/11054281 Publication No. US20060013813A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 324
SOFTWARE: Patentin Ver. 2.1
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US-11-054-281-108
                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-10-821-234-1254
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Best Local Similarity
Matches 51, Conserv
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ORGANISM: Homo sapiens
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Matches 51; Conserv
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LENGTH: 1735
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US-10-495-083-3
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APPLICANT:
APPLICANT:
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General Set Application US/11054281

| Sequence Set Application US/11054281
| Publication No. US20060013813A1
| GENERAL INFORMATION:
| APPLICATION: Processes et al. |
| TITLE OF INVENTION: Processes et al. |
| TITLE OF INVENTION: Processes et al. |
| CURRENT APPLICATION NUMBER: US/11/054,281
| CURRENT APPLICATION NUMBER: US/261,014 |
| PRIOR FILING DATE: 2005-0261,014 |
| PRIOR FILING DATE: 2001-01-11 |
| PRIOR FILING DATE: 2001-01-11 |
| PRIOR FILING DATE: 2001-01-11 |
| PRIOR PLICATION NUMBER: 60/261,018 |
| PRIOR PLICATION NUMBER: 60/261,013 |
| PRIOR PLICATION NUMBER: 60/261,013 |
| PRIOR FILING DATE: 2001-01-11 |
| PRIOR FILING DATE: 2001-01-11 |
| PRIOR FILING DATE: 2001-01-11 |
| PRIOR FILING DATE: 2001-01-11 |
| PRIOR PLICATION NUMBER: 60/261,026 |
| PRIOR PLICATION NUMBER: 60/261,026 |
| PRIOR PLICATION NUMBER: 60/261,026 |
| PRIOR PLICATION NUMBER: 60/261,026 |
| PRIOR PLICATION NUMBER: 60/261,026 |
| PRIOR PLICATION NUMBER: 10/044,564 |
| PRIOR PRING DATE: 2001-08-17 |
| PRIOR PRING DATE: 2002-01-11 |
| PRIOR PRING DATE: 2002-01-11 |
| PRIOR PRING DATE: 2002-01-11 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 106, Application US/11054281 Publication No. US20060013813A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: UNC-13 IN THE MODULATION OF NEUROTRANSMISSION AND SECRETION EVENTFERILE REFERENCE: 009848-0309442

CURRENT APPLICATION NUMBER: US/10/495,083

CURRENT PILING DATE: 2004-05-05

PRIOR PILING DATE: 2002-10-29

PRIOR PILING DATE: 2002-10-29

PRIOR APPLICATION NUMBER: EP 01 12 6235.9
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5.9%; Score 138.5; DB 6; Length 1735;
Best Local Similarity 22.1%; Pred. No. 0.1;
Matches 103; Conservative 59; Mismatches 141; Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                        .5; DB 7; Length 1219; 0.067;
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29.0%; Pred. No. 0.06
tive 35; Mismatches
PRIOR APPLICATION NUMBER: 60/201,02,
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/313,170
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 324
SEQ ID NO 106
SEQ ID NO 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10495083 Publication No. US20060008800A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
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ASHERY, Uri
JUNGE, Harald
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TYPE: PRT
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Publication No. US20050266242A1
GENERAL INFORMATION:
APPLICANT: Lindquist et al.
TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
FILE REFERENCE: 30554/40025A
CURRENT APPLICATION NUMBER: US/11/089,551A
CURRENT APPLICATION NUMBER: US 60/559,286
PRIOR APPLICATION NUMBER: US 60/559,286
PRIOR FILING DATE: 2004-03-31
NUMBER OF SEQ ID NOS: 65
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Sequence 305, Application US/11124368A
Sequence 305, Application US/20050287559A1
GENERAL INFORMATION:
APPLICAMY: Michele Cargill
APPLICAMY: James J. Devlin
APPLICAMY: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CLO01524
CURRENT APPLICATION NUMBER: US/11/124,368A
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                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 NYSLFVSDNLGEQPT-----KCSP--EEDEEDEEDVDDEDHDEGFGSEHELSE- 381
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                                                                                                                                                                                       ----VPSSQCCNWNYFGWGEQNDDPDSA-VDDRDSDY 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ::|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
                                                                                                                                                                                                                                                                                                                                       201 RSETSNSIPPPYYTTSQPNASVHQYSVRP----PPLGSR------ESYSDSMHSYEE
                                                                                                             LPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCVQ-----KASKPPSSTQIMVKTNMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 HNEKVN-----FHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
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Best Local Similarity 30.5%; Pred. No. 0.037;
Matches 36; Conservative 25; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 ELEEEEBLEBEELEEEBEEVPDDLASYTQQEDTTVAEPKRIS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 --NEEEEEEEEDYEDDKDDDISDTF-SEPGYENDSVEDLKEVTSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Saccharomyces cerevisiae US-11-089-551A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-124-368A-305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-11-089-551A-28
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2293 ETTDADKEPAGE---DKGIKALKESAKQTPAPAASVTGSRRRPRAPRESAQAIEDLAGFK 2349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2240 -----SLTAGKATKIPCESPPLEVVDTTASTKRHLRTRVQKVQVKBEPSAVKFTQTSG 2292
                                                                                                                                                                                                                                                                                                                                                                                                 ------SPKÖILDPAASVTGSR 2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 LPQEGPGSLAAGESSSL---SASTSVSDSSQKKEEHNYSLFVSDNLGEQP----TKCSP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 EEDBEDEEDVDDEDHDEGF------GSEHELSENEEREEEBDYEDDK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hongjin Huang
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
GURRENT APPLICATION WUMBER: US/11/124,367A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION WUMBER: US 60/589,609
PRIOR APPLICATION WUMBER: US 60/582,609
PRIOR APPLICATION WUMBER: US 60/599,554
PRIOR APPLICATION WUMBER: US 60/599,554
PRIOR SPECIAL ON BATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 433
LENGTH: 2801
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 QS----RPLLSQIHTDAAKENTCYCGAVAKROEKKGMEPLQGHATPALPFKETQELLLSP
                                                                                                                                                                                                                                                                                                                                                         2 POPSUSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFWYELDREMNYQQNPRDNFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1979 LEDLVGFKELPQTPGHTEESMTDDKITEVSCKSPQPESFKTSRSSKQRLKIPLVKVDMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 DLTKYTKLT-----SCDIWGTKEVDYLGLDDFSSPYQD-BEVISKTPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 AQLNS--EDSQSVSDSLYYPDSLFSV-----KQNPLPSSFPGKKITSRAAAPVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 SSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |::||:|
2350 D-----PAAGHTEESMIDDKTIKIPCKSSPELEDTAISSKRRPRTR 2390
                                                                                                                                                                                                                                               5.6%; Score 132.5; DB 7; Length 2801; 20.8%; Pred. No. 0.46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      397 DDDISDTFSEPGYENDSVEDLK------EVTSISSRKRGKRR 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 LEDCKDIENL-----ESFTDVLDNEGALTS-NWEQWDT
                                                                                                                                                                                                                                                                                 ; Pred. No. 0.46;
65; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2039 EPLAVSKLTRTSGETTOTHTEPTGDSKSIKAFKE
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 305
LENGTH: 2801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 433, Application US/11124367A; Publication No. US20060024700A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 20.8%
Matches 110; Conservative
                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-11-124-368A-305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-124-367A-433
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; ORGANISM: Homo sapiens US-11-124-367A-433

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2039 EPLAVSKITRISGETTQTHTEPTGDSKSİKAFKE------SPKQILDPAASVTGSR 2088
                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                        -----SCDIWGTKEVDYLGLDDFSSPYQD-EEVISKTPTL 139
                                                                                                                                                                                                                                                                                                                                           187 SSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 LPQEGPGSLAAGESSSL---SASTSVSDSSQKKEEHNYSLFVSDNLGEQP----TKCSP 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 EEDEEDEEDVODEDHDEGF------GSEHELSENEEBEEEBEPOK 396
                                                                                                                                                                                                                                                                            140 AQLNS--EDSQSVSDSLYYPDSLFSV------KQNPLPSSFPGKKITSRAAAPVC 186
                                                                                                                                                                                                                                                                                                                                                                                                               247 QS----RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSP 302
                                                                   2 POPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYOONPRDNFLS 61
                                                                                                                                      62 LEDCKDIENL-----ESFTDVLDNEGALTS-NWEQWDT------YCE 96
Query Match 5.6%; Score 132.5; DB 7; Length 2801; Best Local Similarity 20.8%; Pred. No. 0.46; Matches 110; Conservative 65; Mismatches 184; Indels 169; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : : | : | | D-----PAAGHTEESMTDDKTTKIPCKSSPELEDTATSSKRRPRTR 2390
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Search completed: February 28, 2006, 09:02:40 Job time : 13.9766 secs

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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                Copyright
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OM protein - protein search, using sw model

Run on:

February 28, 2006, 08:45:35; Search time 27.3216 Seconds (without alignments) 1577.691 Million cell updates/sec

US-10-717-665A-44_COPY_1_448 Title: Perfect score:

2364 1 MPQPSVSGMDPPFGDAFRSH......GKRRYFWEYSEQLTPSQQER 448 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR 80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		þ				
Result		Query				
No.	Score	Match	Length	2000	OI	Description
-	188.5	8.0	707	н	DNMS	nucleolin - mouse
7	185.5	7.8	712	~	JH0148	nucleolin - rat
٣	178.5	7.6	2761	7	T29285	•~
4	165	7.0	678	7	A54514	
Ω.	165	7.0	707	~	A35804	nucleolin - human
9	162	6.9	1187	7	T46637	transcription fact
7	161	6.8	831	7	S39835	hypothetical prote
80	160.5	6.8	1974	~	T16703	
0	159.5	6.7	1128	~	G86266	hypothetical prote
10	157	9.9	562	~	S38149	
11	153	6.5	792	7	T42963	hypothetical prote
12	152.5	6.5	200	7	S55785	nucleolar protein
13	152.5	6.5	896	7	T24169	hypothetical prote
14	152.5	6.5	906	7	T24166	
15	152	6.4	1038	~	S52522	hypothetical prote
16	152	6.4	1182	0	T30189	myelin transcripti
17	151.5	6.4	740	7	T03847	Fas-binding protei
18	151.5	6.4	1188	N	T46608	
19	150.5	6.4	669	~	T01029	cal
20	150.5	6.4	713	N	A27441	nucleolin - Chines
21	150.5	6.4	797	N	A36811	hypothetical prote
22	149	6.3	1063	~	A40253	acidic nuclear pro
23	149	6.3	1262	7	T33074	hypothetical prote
24	148.5	6.3	1089	~	S48244	NMD2 protein - yea
25	148.5	6.3	1094	N	S49313	protein kinase - s
26	148.5	6.3	1300	7	T03166	probable immediate
27	148	6.3	972	N	T49773	
28	147	6.2	3724	~	T18427	U
29	146.5	6.2	727	~	JC5113	ribosomal transcri

F;397-402/Region: RNA-binding RNP2 motif F;431-438/Region: RNA-binding RNP1 motif F;488-551/Domain: ribonucleoprotein repeat homology <RRM3> F;488-494/Region: RNA-binding RNP2 motif

F:311-316/Region: RNA-binding RNP2 motif F:349-356/Region: RNA-binding RNP1 motif F:396-458/Domain: ribonucleoprotein repeat homology <RRM2>

ribosomal transcri	nestin - golden ha	nucleolin - chicke	transcription fact	neurofilament prot	fibrinogen-binding	immediate-early pr	hypothetical prote	probable transcrip	IFH1 protein - yea	hypothetical prote	probable secreted	transcription acti	probable TPR repea	ASF1 protein - yea	transcription init
JC5112	T34518	DNCHNL	S17196	T52485	S41539	EDBEQ3	T15094	T38274	S55352	E86336	A71623	T30967	B84476	330766	S37845
N	N	н	~	'n	~	~	~	N	~	N	~	N	N	7	7
764	1804	694	701	913	933	407	553	990	1085	409	1192	1100	1115	279	482
6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.1	6.1	6.1	6.1	9	0.9	9	0.9
146.5	146.5	146	146	146	146	145.5	145.5	145	145	144.5	144.5	143	143	142.5	142
	_	~	m	4	S	9	7	8	6	0	_	~	e	4	Z.

## ALIGNMENTS

```
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: No. 869-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
CiAccession: A29588, A40769; A5640; 184688
R;Bourbon, H.M.; Lapeyre, B.; Amalric, F.
J. Mol. Biol. 200, 627-638, 1988
A;Title: Structure of the mouse nucleolin gene. The complete sequence reveals that each FA;Reference number: A29958; MUID:88316930; PMID:3137346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A;Residues: 2-20, %7, 22-24 cPAS>
A;Cross-references: UNIPARC:UP100001739CF
R;Yang, T.H.; Tsai, W.H.; Lee, Y.M.; Lei, H.Y.; Lai, M.Y.; Chen, D.S.; Yeh, N.H.; Lee, S.
Mol. Cell: Biol. 14, 6068-6074, 1994
A;Title: Purification and characterization of nucleolin and its identification as a trank
A;Reference number: A56240; MUID:94344117; PMID:8065340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT: P09405; UNIPARC:UP100000009C3; GB:X07699; NID:g53453; PIDN:C? R;Pasternack, M.S.; Bleier, K.J.; McInerney, T.N. J. Biol. Chem. 266, 14703-14708, 1991
A;Title: Granzyme A binding to target cell proteins. Granzyme A binds to and cleaves nucl A;Reference number: A40769; MUID:91317840; PMID:1860869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 68, 73-84, 1988
Gene 68, 73-84, 1988
A, Title: Sequence and structure of the nucleolin promoter in rodents: Characterization of
A, Reference number: 148118; MUID:89121496; PMID:2906027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UP1000016CF68; GB:M22089; NID:g200111; PIDN:AAA39841.1; PID:c
C;Comment: This housekeeping protein is involved in the synthesis, packaging, and maturat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Intrones: 6/3; 45/3; 211/1; 273/1; 302/1; 349/2; 391/1; 432/3; 484/1; 525/2; 566/1; 608/
C; Superfamily: nucleolin; ribonucleoprotein repeat homology
C; Keywords: DNA binding; duplication; nucleus; phosphoprotein; RNA binding; transcriptior
F; 310-375, Domain: ribonucleoprotein repeat homology <RRM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Wolecule type: protein
A;Residues: 2-19;558-567 <YAN>
A;Cross-references: UNIPARC:UP100001739D0; UNIPARC:UP100001739D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-44 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-707 <BOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: I84688
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RESULT 1
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2

11;

Gaps

362

---GFGSEHELSENEEEEEE

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A;Gene: CESP:C34D4.14
A;Map position: 4
A;Introns: 120/1; 201/3; 365/3; 445/2; 509/1; 728/3; 856/3; 902/3; 940/3; 1027/3; 1508/3;
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A;Cross-references: UNIPROT:Q18447; UNIPARC:UP1000007762A; EMBL:U58755; PIDN:AAB00699.1;
A;Experimental source: strain Bristol N2; clone C34D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1668 NRH--------KOHNKPAASALSRFASVKNTTPAGTPSSGGSSGGAIGKKSM 1711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 EDEEDEEDDEDEEEEEEPVKAAPGKRKKEMTKQKEAPEAKKQK------IEGSEPTT 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390 EDYEDDKDDDISDTFSE-----PGYENDSVEDLKEVTSISSRKRGKRRYFWEYSEQLT 442
                                                                                                                                                                                                                                                        129 DEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein C34D4.14 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                    189 KTLQAEVPLSDCVQKASKPPSSTQIMVKTNNYHNEKVNFHVECKDYVKKAKVKINPVQQS
                                                                                                                                                                                                                                                                                                  249 RPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 GSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP-----EEDEEDEE
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                                                                                                                                            Query Match 7.8%; Score 185.5; DB 2; Length 712; Best Local Similarity 23.3%; Pred. No. 0.003; Matches 84; Conservative 34; Mismatches 134; Indels 109;
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7.6%; Score 178.5; DB 2; Length 2761;
Best Local Similarity 21.6%; Pred. No. 0.039;
Matches 84; Conservative 53; Mismatches 116; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GKKGAAQAKALVPTPGKKGA-----VTPAKGAKN----
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F;311-376/Domain: ribonucleoprotein repeat homology «RRM1» R;397-459/Domain: ribonucleoprotein repeat homology «RRM2» F;489-552/Domain: ribonucleoprotein repeat homology «RRM3» F;575-639/Domain: ribonucleoprotein repeat homology «RRM3»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T29285
R;Du, Z.; Le, T.T.
submitted to the EMBL Data Library, May 1996
A;Description: The sequence of C. elegans cosmid C34D4, A;Reference number: Z20600
A;Reference number: T29285
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 23-Jul-1999
C;Accession: JH0148; A24088; <u>T</u>63130
R;Bourbon, H.M.; Amalric, F.
Gene 88, 187-196, 1990
A;Title: Nucleolin gene organization in rodents: highly conserved sequences within three A;Reference number: JH0148; MUID:90269607; PMID:2347493
A;Accession: JH0148
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A;Residues: 'MV',2-44 <RES>
A;Cross-references: UNIPARC:UPI0000170A72; GB:M22090; NID:g205793; PIDN:AAA41733.1; PID:
C;Comment: This protein is the major nucleolar-specific protein in eukaryotic exponentia
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A,Title: Sequence and structure of the nucleolin promoter in rodents: Characterization A,Reference number: 148118; MUID:89121496; PMID:2906027
A,Accession: 163130
A,Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-712 <BOUS
A; Residues: 1-712 <BOUS
A; Cross-references: UNIPARC:UPI000017723A
A; Cross-references: UNIPARC:UPI000017723A
A; Note: the authors translated the initiation codon GTG for residue 1 as Val
R; Lischwe, M.A.; Cook, R.G.; Ahn, Y.S.; Yeoman, L.C.; Busch, H.
Biochemistry 24, 6025-6028, 1985
A; Title: Clustering of glycine and Ng, Ng-dimethylarginine in nucleolar protein C23.
A; Reference number: A24088; MUID:86104094; PMID:4084504
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                                                                                                                                                                                                                                                                                                                                                                                   197 LSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIH 256
                                                                                                                                                                                                                                                                                                                                                                                                                                            76 TP--AKKAAVTPGK------ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 IDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLP-QEGPGSLAAGE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AAQAKALVPTPGKKGAATPAKGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 SSSLSASTSVSDSSQKKEEHNYSLFVSDN------LGEQPTKCSP----EEDEED 360
                                                                                                                                                                                                                                                                    137 PTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVCSSKTLQAEVP 196
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                                                                                                                                                                                                                                                                                                                       21 PKEVEEDSEDEEMSEDE----DDSSGEEEVVIPQK-KGKKATTTPAKKVVVSQTKKAAVP
                                                                                                                                                  Query Match
8.0%; Score 188.5; DB 1; Length 707;
Best Local Similarity 23.5%; Pred. No. 0.002;
Matches 84; Conservative 40; Mismatches 113; Indels 121; Gaps
              F;524-531/Region: RNA-binding RNP1 motif
F;570-634/Domain: Tibonucleoprotein repeat homology <RRM4>
F;571-576/Region: RNA-binding RNP2 motif
F;607-614/Region: RNA-binding RNP1 motif
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A,Residues: 651-703 <LIS>
A,Cross-references: UNIPARC:UP1000017723B
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R;Jordan, P.; Heid, H.; Kinzel, V.; Kuebler, D.
Biochemistry 33, 14696-14706, 1994
A;Title: Major cell surface-located protein substrates of an ecto-protein kinase are hom
A;Reference number: A55996; MUID:95086063; PMID:7993898
                                                                                                                                    UNIPARC:UPI0000161B7E; GB:M60858; GB:J05584; NID:g185
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X,Residues: 211-236;349-362;399-403;458-461;655-656,'X',658-660 <JOR>
A;Cross-references: UNIPARC:UPIO000177236; UNIPARC:UPI000017723D; UNIPARC:UPI000017723E;
A;Experimental source: surface-labelled HeLa cells
                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-707 -68R2-
A;Cross-references: UNIPARC:UPI0000161B7E
A;Fishikawa, F.; Matunis, M.J.; Dreyfuss, G.; Cech, T.R.
Mol. Cell. Biol. 13, 4301-4310, 1993
A;Title: Nuclear proteins that bind the pre-mRNA 3' splice site sequence r(UUAG/G)
A;Reference number: A48138; MUID:993309464; PMID:8321232
            A:Title: Genomic organization and chromosomal localization of the human nucleolin A;Reference number: A35804; MUID:90368666; PMID:2394707
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22.0%; Pred. No. 0.043;
tive 52; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: DNA binding; nucleolus; nucleus; phosphoprotein;
C;Keywords: DNA binding; nucleolus; nucleus; phosphoprotein;
F;308-373/Domain: ribonucleoprotein repeat homology «RRM1>
F;334-456/Domain: ribonucleoprotein repeat homology «RRM3>
F;573-634/Domain: ribonucleoprotein repeat homology «RRM4>
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                                                                                                                                                                                         A; Title: Cloning and sequencing of the human nucleolin cDNA. A; Reference number: S04631; MUID:89290043; PMID:2737305 A; Accession: S04631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Note: sequence extracted from NCBI backbone (NCBIP:134645)
                                                                                                           A;Reduces: 1-707 <SRI>
A;RCOSB-references: UNIPROT:P19338; UNIPARC:UPI0000161B7E; (R;Srivastava, M.; Fleming, P.J.; Pollard, H.B.; Burns, A.L. FEBS Lett, 250, 99-105, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 2q12-2qter
C;Superfamily: nucleolin; ribonucleoprotein repeat homology
                                                                                                                                                                                                                                                                                   A;Status: not compared with conceptual translation
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A;Residues: 458-474 <ISBN-
A;Cross-references: UNIPAC:UP10000073927
A;Experimental source: HeLa cell nuclei
J. Biol. Chem. 265, 14922-14931, 1990
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                                                                                            A, Molecule type: DNA
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                                                                   A; Accession: A35804
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Best Local S:
Matches 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-678 <TRI>
A;Cross-references: UNIPROT:P13816; UNIPARC;UP1000012B0E0; GB:J03998; NID:g160298; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: A54514
R;Triglia, T.; Stahl, H.D.; Crewther, P.E.; Silva, A.; Anders, R.F.; Kemp, D.J.
Mol. Biochem. Parasitol. 31, 199-202, 1988
A;Title: Structure of a Plasmodium falciparum gene that encodes a glutamic acid-rich
A;Reference number: A54514; MUID:89040048; PMID:2903445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                       1883 DEEDDDDDDDDDDSSNENQEKLVELLGGERGLFDKLKEVITGESLSDASSSAKDATINEAQ 1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510
1712 STINLVDERQKTSGPSVASTGQAASAESLQ-HQTPSL----ENLLARAMPHAFGRIAEN 1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glutamic acid-rich protein precursor - malaria parasite (Plasmodium falciparum)
N;Alternate names: GARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 GKKITSRAAAPVCSSKTLQAEV-PLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVE-- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------EDEEDVDDED---HDEGFGSEHELSENEEEEEEE 390
                                                                                                                                                                                                                                           ----TSISS 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
jbate: 23-Oct-1990 #text_change 09-Jul-2004
jAccession: 315804; S04631; R48138; R5596
strivascava, M.; McBride, O.W.; Fleming, P.J.; Pollard, H.B.; Burns, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------CKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVEIINLEDKEACEEQHITVESRPLSQPQCKLIDEPEQLTLMDKSKV---EEKNLSIQEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFVSDNLGEQPTKCSPEEDEEDVDDEDHDEGFGSEHELSENEEEEEEEDYEDDKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQE------ESKEVQE------BEEVEBDEBEBEBEBEEEE
                                                  ---TSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.Alternate names: GARP
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.0%; Score 165; DB 2; Length 67
22.3%; Pred. No. 0.041;
tive 44; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-DDEDEDEDEBEEEEEEEEEEEKKIKRNLRK 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399 DISDTFSEPGYENDSVEDLKEVTSISSRKRGKRR 432
                                                                                                                                                                                                                                              DYEDDKDDDISDTFSEP-----GYENDSVEDLKEV
                                                                                                                                                                                                                                                                                                                                                                      1943 KKGGKKPKKPKKMSSYTDVLKGLMQNR 1970
                                                                                                                                                                                                                                                                                                                                          426 RKRGKRRYFW----EYSEQLTPSQQER 448
                                                    305 QEGPGSLAAGESSSLSAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                 355 EEDE-----
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C;Keywords: tandem repeat
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Best Local 3
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Matches
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Gaps

----- LQAEVPLS 198

A; Map position: 2L

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A,Accession: T16703
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-1974 <CON>
A,Cross-references: UNIPROT: Q09612; UNIPARC: UPI000008390B; EMBL: U23452; NID: g733564; PID: A,Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: CESP:R07G3.3
A;Introns: 91/3; 158/3; 244/3; 480/3; 574/3; 722/2; 759/3; 913/2; 948/2; 1114/3; 1323/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1475 TSQQPPSFAAKRPSFGRQAQSSSNVIPPAPAPTPTSQQKVSPVKRPIPPSIPNEPLDIIP 1534
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                                                                                                                                                                                                                                                                                                              142 LN-----SEDSQSVSDSLY-----YP----DSL-----FSVK--QNPLPSSF 172
                                                                                                                                                                                                                                                                                                                                                                      107 CDIWGTKEVDYLGLDDFSSPYQDEEVISKTPT--LAQLNSEDSQSVSDSLYYPDSLFSVK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---STQI---MVKTNMY------HNEKVNFHVECKD-YVKKAKVKINPVQQSRPLLSQI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199 DCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 AAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFK-FTQ-ELLLSPLPQEGPGSLAAGES 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------DRKGI------PRSKFSTETHWELCFTIKNSETP----LGNH 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 SSLSASTSVSDSSQXKEEHNY--SLFVSDNLGEQPTKCSPEEDEEDVDDEDHDEGFG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 SEHELSENEREEEEEEEDYEDDKDDISDTFSEPGYENDSVEDLKEVTSISSRKRGKRR 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein R07G3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                : :|: || |: |
594 ADEALTNETMAPVISNNTHIENYNNSRAHNKRRRRRSSEHKTSKLHVNNIIEPEVPAT
                                                                                                                                                         86 SNWEQWDTY----CEDLTKYTKLTSCDIWGTKEVDYLGLDDFSSPYQDEEVISKTPTLAQ
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6.8%; Score 160.5; DB 2; Length 1974;
Best Local Similarity 21.6%; Pred. No. 0.27;
Matches 104; Conservative 51; Mismatches 152; Indels 175;
                                                                                  62; Mismatches 116; Indels 154;
6.8%; Score 161; DB 2; Length 831; 20.6%; Pred. No. 0.089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: T16703
R;Connell, M.
Bubmitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid R07G3.
A;Reference number: Z18562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 PGKKITSRAAAPVCSSKT----
           Query Match
Best Local Similarity 20.65
Matches 86; Conservative
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N;Alternate names: hypothetical protein YBL0507; hypothetical protein YBL0515
N;Alternate names: hypothetical protein YBL0507; hypothetical protein YBL0515
C;Species Saccharomyces cervisian
C;Date: 16-Dec-1993 #sequence revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: S39835; S45787; S37336
C;Accession: S39835; S45787; S37336
A;Scherns, B.; el Bakkcury, M.; Vierendeels, F.; Dubois, E.; Messenguy, F.
Yeast 9, 1355-1371, 1993
A;Title: Sequencing and functional analysis of a 32 560 bp segment on the left arm of year sequence number: S39824; MUID:94205266; PMID:8154187
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A;Cross-references: UNIPARC:UPI000135570; EMBL:Z35814; NID:g536078; PIDN:CAA84873.1; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ם
                                                                                  Transcription factor 1, neural - rat

N;Alternate names: neural zinc finger factor-1

N;Alternate names: neural zinc finger factor-1

C;Species: Rattuen norvegicus (Norway rat)

C;Species: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004

C;Accession: T46637

C;Accession: T46637

C;Accession: T46637

C;Accession: T46637

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: UNIPROT:P70475; UNIPARC:UPI00000E86A7; EMBL:U48809; NID:g1511631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain S288C
R; Dubois, E.; El Bakkoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens,
submitted to the Protein Sequence Database, August 1994
A; Reference number: S45782
A; Accession: S45787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: UNIPROT:P34218; UNIPARC:UP10000135570; EMBL:Z23261; NID:9313733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 DECYESDGTEDMODKEEDDDEEFSEDNDEQGDDDDEDEVDREDEEEIEEBDDEDDDD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 GDDVEEEEDDDDDEEEEEEEEEEEEEENDDHWODEYDNYDELVAKSLL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 AKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 SA--STSVSDSSQKKEEHNYSLFVSDNLGEOPTKCSPEEDEEDEEDV-----DDEDHDE 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 GFGSEHELSENEEEEEEEEDYEDDKDDDISDT--PSEPGYE---NDSVEDLKEVTSISSR 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 ARHRSVYGCPLAKKRKTQDKQP-----QP----PAPKRKPFAVKA-DSSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%; Score 162; DB 2; Length 1187; ilarity 28.3%; Pred. No. 0.12; Conservative 35; Mismatches 65; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1187 <JIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene: SGD:SAS3
Cross-references: SGD:S0000148; MIPS:YBL052c
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Best Local Similarity
Matches 52; Conserv
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A; Residues: 1-831 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 KRGK 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: NZF-1
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q	1535 PVPSDNIPDPTPPTNSFGTVLPVPHTFQTSVRVPTQSLFSSSSTTTVQPQPEKGNVLPSI 1594	Db 970 HIDDTATGGKRRRQCTVAVLPQTPGQRHYNLRRKKTVDQVPADVEDNAAGE 1021
දු පු	256 HTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGFG 309	316 -SSSLSASTSVSDSSQ
è a	310 SLAAGESSSLSASTONSDSSQKKEEHNYSLFVSD 343	365 DDEDHDEGFGSEHELSENEEBEEBEBYEDDKDDISDTSBPG 408
हे ह	344 NLGEOPTKCSPEEDEED	1082 UEEEDEAQUOUNEENQUOUUUUUUGUUGGGGGGGGGGGGGGGGGGGGGGGGGGG
3 &	EDVDDEDHDEGPGSEHELSENEEEEEEDVEDDIT	S38149 SIS2 protein - yeast (Saccharomyces cerevisiae) N'alternate names: protein YKR072c
qa .		C.Species: Saccharomyces cerevisiae C.Species: Saccharomyces cerevision 03-May-1994 #text_change 09-Jul-2004
රු සි	419 EV 420 :: 1820 DI 1821	CyAccession: 39017. STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STOCK, STO
RESULT	0	A, Accession: 33119 A, Molecule type: DNA A, Molecule type: DNA
G86266 hypothe C;Speci	tical protein F3F19.25 - Arabidopsis thaliana es: Arabidopsis thaliana (mouse-ear cress)	A; Kesidues: 1-562 < POLY A; Cross-references: UNIPROT: P36024; UNIPARC: UPI00001359B5; EMBL: Z28297; NID: 9486544; PID: A; Experimental source: strain 3288C
C, Date: C, Acces R, Theol	C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: G86266 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chir, Chira, M.Y., Chan, T., Chansy, A.P., Chansy, A.P., Chask, T.H.; Dawar, K.;	Kjul Como, C.10.; 2005, A.; Aller, A.; Genetics 139, 95-107, 1995 Genetics 139, 95-107, 1995 A,Title: Overexpression of SIS2, which contains an extremely acidic region, increases the A,Reference number: S54982; MUID:95220693; PMID:7705654
ansen,	C.W.; Chung, M.K.; Conn., L.; Conway, A.B.; Conway, A.K.; Creasy, A.M.; Conc., C. A.A., A.B.; Hulzar, L. A.A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A.B.; A	A;Accession: S54982 A;Molecule type: DNA
A, Author C.A.; I	rs: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. ii, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,	A;Residues: 1-562 <diw> A;Residues: 1-562 <diw> A;Cross-references: UNIPARC:UPI00001359B5; EMBL:U01878; NID:g430983; PIDN:AAA80000.1; PII</diw></diw>
Rizzo, A;Authc ker, M. A;Title	Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.	A;Gene: SGD:SIS2 A;Cross-references: SGD:S0001780; MIPS:YKR072c A;A;App position: 11R
A;Refe1 A;Acce£	rence number: A86141; MUID:21016719; PMID:11130712 98ion: G86266	
A;Stati A;Molec		Query Match 6.6%; Score 15/; UB 2; Length 562; Best Local Similarity 20.5%; Pred. No. 0.093; Matches 86; Conservative 64; Mismatches 120; Indels 150; Gaps 15;
A; Cross C; Genet A; Map E	;Cross-references: UNIPROT:Q9SAF6; UNIPARC:UP100000A7DC7; GB:AE005172; NID:g4850405; PI ;Genetics: ;Map position: 1	QY 113 KEVDYLGLDDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFS 162       :
Query Ma Best Loc Matches	Ouery Match  6.7%; Score 159.5; DB 2; Length 1128;  Best Local Similarity 23.3%; Pred. No. 0.16;  Marches 108: Conservative 65; Mismatches 176; Indels 115; Gaps 23;	163
કે ક	33 LANSSDEDFMYE-LDREMNYQQNPRDNFLSLEDCE 	
8 8		Db 284 KKLBEIYGRDRISIQV
요 :	733 LSTLSINLKKRREVFGRERSRFLAFVQKLKDCGSCGQLVNDFV-LSDLQLPSNDEVAL 789	37
දු පු		Qy 296QELLLSPLPQEGPGSLAAG
<u>ک</u> ۾	190TLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVE 230	330
ò	231CKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENT 264	41
QQ		:    :    :
È	265CYCGAVAKROEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGE 315	

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Anolecule type: DNA
A;Residues: 1-338, 'S', 340-500 <BRO>
A;Cross-references: UNIPARC: UPI000012B0DD; EMBL: Z99091; PIDN: CAB11772.1; GSPDB: GN00066; & A;Experimental source: strain 972h-; cosmid c13F5
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-896 <WIL>
A;Cross-references: UNIPROT:062348; UNIPARC:UPI00007DBCA; EMBL:Z83122; PIDN:CAB05601.1;
A;Experimental source: clone R11A5
A, Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 EDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSRAAAPVC--SSKTLQAEVPLSDCVQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 KASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377 HELSENEEEEEEEEEDYEDDKD------DDISDTFSEPGYENDSVEDLKEVTSISSRK 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 SSSSESEEEEEVVEXTEEKKEGSSESSDSESSSSSSSG-DSDSSSDSESSSSEK 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein R11A5.1b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24169
R;McMurray, A.
submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 NTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 TSVSD-----SSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KDKTSVKKSVKETAS----KKGAIEKPSKSKKITKEAAKEIAKOSSKT-----DVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
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                           A;Molecule type: mRNA
A;Residues: 374-407 <VAN>
A;Cross-references: UNIPARC:UPI000017A376
K;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood,
submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 1
A;Introns: 14/2; 40/3; 277/3; 308/3; 353/3; 550/1; 658/1; 798/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 1
F;264-331/Domain: ribonucleoprotein repeat homology <RRM1>
F;367-433/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.5%; Score 152.5; DB 2; Best Local Similarity 23.4%; Pred. No. 0.15; Matches 75; Conservative 38; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: 219848
A;Accession: T24169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guery Match
6.5%; Score 152.5; I
Best Local Similarity 32.3%; Pred. No. 0.3;
Matches 43; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                428 RGKRRYFWEYSEQLTPSQQER 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 KRKAE------PASEER 248
                                                                                                                                                                                                                                                                                                                                                                        A; Gene: gar2; SPDB:SPAC13F5.09
                                                                                                                                                            A; Reference number: Z21733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Gene: CESP:R11A5.1b
                                                                                                                                                                                        A; Accession: T37634
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Curr. Genet. 29, 307-315; 1996
A;Title: Molecular analysis of a novel Schizosaccharomyces pombe gene containing two RNF A;Reference number: S68083; MUID: 96171513; PMID: 8598051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleilar protein gar2 - fission yeast (Schizosaccharomyces pombe)

NyAlternate names: probable RNA-binding protein RBD18

C;Species Schizosaccharomyces pombe

C;Species Schizosaccharomyces pombe

C;Batc: 28-Oct-1996 #sequence revision 07-Feb-1997 #text_change 05-Oct-2004

C;Accession: S55785; 868087; T37634; S52318

R;Gulli, M.P.; Girard, J.P.; Zabetakis, D.; Lapeyre, B.; Melese, T.; Caizergues-Ferrer,

Nucleic Acids Res. 23, 1912-1918, 1995

A;Title: gar2 is a nucleolar protein from Schizosaccharomyces pombe required for 18S rRN

A;Reference number: S55785; MUID:95319932; PMID:7596817

A;Status; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                      A;cross-references: UNIPROT:09xTL7; UNIPARC:UPI00000EC1E3; EMBL:AF083424; PIDN:AAC95573 A;Experimental source: strain 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 KVGKNSL--NRKYLENL-KDNKRKNNNYSGRNNKYKGDGANDKDKSIDKNESEGGDHSEI 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 HATPALPFKETQELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDN 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 KUKINPVQQSRPLLSQIHTDAAKENTCYCGAVAK-------RQEKKGMEPLQG 284
                                                 C.Species: ateline herpesvirus 3 (strain 73)
A;Variety: strain 73
C;Date: 21-Jān-2000 #sequence_revision 21-Jān-2000 #text_change 09-Jul-2004
R;Albrecht, J.C.: Flackenser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 WGTKEVDYLGLD--DFSSPYQDEEVISKTPTLAQLNSEDSQSV-SDSLYYPDSLFSVKQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 SILGSRGIGLDLFRTQDVLKFPSSDAKFMAVSQPDNFNEKEVEFSMTGGKTDSEDVTAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : : | : | | | | | 410 NREKNRKRKKPNGFRVGDKEVGEEKSVKSGEGKK-SEKDSEEBAEDKDEEEN----KKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 LGEQPTKCSPEEDEEDEEDVDDEDHDEGFGSEHELSENEEEEEEEEDYEDDKD-DDISDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 PLPSSFPG-KKITSRAAAPVCSSKTLQAEVPLSDCV--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76; Gaps
                                                                                                                                                                                     Length 792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.5%; Score 153; DB 2; Length 79. Best Local Similarity 22.6%; Pred. No. 0.24; Matches 85; Conservative 62; Mismatches 153; Indels
                                                                                                                                                                                                                                                                                                                      A,Accession: T42963
%Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-792 <ALB>
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524 EDEEDEEDEEEEDEE 539
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A; Residues: 1-500 <GUL>
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647 EAWSKKISSSPWWCFA-----KNVSKFDGSDNSILPEGAFRLKNENDQNHLP---PAQ 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 VOKASKPPSSTQIMVK----TNMYHNEKVNFHVECKDYVKKAKVKINPVQQSRPLL---S
                                                                                                                                                                                                                                                                                                                                          254 QIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALP---FKETQELLLSPLPQEGPGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 LAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPEEDEEDEEDVDDEDHD
                                                                                                                   Query Match 6.4%; Score 152; DB 2; Length 1038; Best Local Similarity 24.8%; Pred. No. 0.38; Matches 61; Conservative 40; Mismatches 89; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: February 28, 2006, 08:54:18 Job time : 28.3216 secs
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A;Cross-references: SGD:S0005930
A;Map position: 16L
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I,Cross-references: UNIPROT:Q12532; UNIPARC:UP10000052E40; EMBL:Z48483; NID:g683777; PID
I,Experimental source: strain AB972
I,Hall, J; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; Wa submitted to the EMBL Data Library, August 1995
I,Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
A;Reference number: S59677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .Molecule type: DNA
.Residues: 1-1038 <HAL>
.Cross-references: UNIPARC:UPI0000052E40; EMBL:U33335; NID:9965076; PID:9965084; MIPS:Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Gross-references: UNIPROT: 045718; UNIPARC:UP10000083395; EMBL: 283122; PIDN: CAB05598.1;
Experimental source: clone R11A5
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1/Alternate names: hypothetical protein LPA8c; hypothetical protein YP8132.04c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 QELLLSPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEHNYSLFVSDNLGEQPTKCSPE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            541 EEIFMSKKP-----APELISSFKEPTS-SDSLLRKEAHAPNELKLDDSDEE--EDDDD 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 EDEEDEEDVDDEDHDEGFGSEHELSENEEEEEEDYEDDKDDISDTFSEPGYENDSVE 415
                                                                                                                                                                                        Species: Saccharomyces cerevisiae
Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
Accession: S52522; S59684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ypochetical protein R11A5.la - Caenorhabditis elegans | Species: Caenorhabditis elegans | Species: Caenorhabditis elegans | Species: L5-Oct-1999 #text_change 09-Jul-2004 | Species: L5-Oct-1999 #text_change 09-Jul-2004 | Species: L5-Oct-1999 #text_change 09-Jul-2004 | Species: L5-Oct-1999 #text_change 09-Jul-2004 | Species L5-Oct-1999 #text_change 09-Jul-2004 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-Oct-1999 | Species L5-
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A;Introns: 14/2; 40/3; 277/3; 318/3; 363/3; 560/1; 668/1; 808/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: T24166
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
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ubmitted to the EMBL Data Library, February 1995; Reference number: S52519
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638 EEKPNPKPSTKKQ 650
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Q5KMZ9_CRYNE Q5CVUZ_CRYPV Q54V59_DICDI Q7RIET_PLAYO Q55SC9_CRYNE Q9C2H4_NEUCR Q7RPC8_PLAYO Q7RY51_NEUCR Q81510_PLAP7 Q4WPX_ASPFU Q4WSA4_PLAF7 Q4WSA4_PLACH Q95XW8_CAEEL	ALIGNMENTS  PRT, 639 AA.  Created)  Last sequence update)  6, Last annotation update)	Craniata; Vertebrata; catioglires; Primates; Cat SMBL/GenBank/DDBJ datab ; UNKNOWN 1.	; Score 2356; DB 2; Length ; Pred. No. 4e-113; 0; Mismatches 1; Indels	MPOPSVSGMDPPFGDAFRSHTFSEQTLANSTDLLANSSDPDFMYELDREMNYQQNPRDNFL 	SLEDCKDIENLESFTDVLDNEGALTSNWEGWDTYCEDLTKYTKLISCDIMGTKEVDYLGL 	DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSPGKKITSR 	aaapucssktiqaevplsdcvqkaskppsstoimvktnmythnekvnfhueckdyvkkakv 	KINDVQQSRPLLSQIHTDAAKENTCYCGAVAKRQBKKGMBPLQGHATPALPFKETQELLL
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	AN PRE	retina procein. yota, Metazoa; Chordata, lia; Eutheria; Euarchond TaxID=9606; OTIDE SEQUENCE. , Yao K.T.; tted (AUG-2002) to the I AY1390008; ARAN89956.1; Pro; IPR004827; TF bZIP TE; PS00036; BZIP BASIC. INCE 639 AA; 72090 MW.	milari Cons	POPSVS        POPSVS	LEDCKD 	DFSSPY        DFSSPY	AAPVCS        AAPVCS	INPVOC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 DDFSSPYQDEEVISKTPTLAQLNSEDSQSVSDSLYYPDSLFSVKQNPLPSSFPGKKITSR 180
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                                                                                                                                                                                                                                                  Name=LOC153222;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
TISSUE-Lung;
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas,242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.7%; Score 2156; DB 2; Length 639; 99.8%; Pred. No. 4e-113; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041709; AAH4709.1; -; mRNA.
Ensembl; ENSG0000164463; Homo sapiens.
InterPro; IPR004827; TF bZIC.
PROSITE; PS00036; BZIP BASIC; UNKNOWN 1.
SEQUENCE 639 AA; 72118 MW; ECFB92D9290DEDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                    639 AA
                      421 TSISSRKRGKRRYFWEYSEQLTPSQQER 448
TSISSRKRGKRRYFWEYSEQLTPSQQER
                                                                                                                                                                        Created)
                                                                                                                                QBIURG HUMAN PRELIMINARY;
QBIURG;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
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Matches 447; Conservative
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Director MGC Project;
                                                                                                                                                                                                                                  Adult retina protein.
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                 1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQUPRDNFL
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The German cDNA Consortium;
Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.5%; Score 2353; DB 2; Length 604; 99.6%; Pred. No. 5.4e-113; tive 1; Mismatches 1; Indels
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Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BX647573; CAI46104.1; -; mRNA.
InterPro; IPR004827; TF bZIP.
PROSITE; PS00036; BZIP_BASIC; UNKNOWN_1.
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604 AA; 68572 MW; 977C229B63E2E4C2 CRC64;
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp313F2319 (Fragment).
Mame=DKFZp513F2319, DKFZp313F2319 (Fragment).
Homo sapiens (Luman).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                     TSISSEKRGKRRYFWEYSEQLTPSQQER 448
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QSHYKO;
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Senome Res. 10:1617-1630(2000).
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XX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

XX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

XX ATAGWAR A., Shibata K., Yoshino M., Ischi Y., Ishi Y., Atagwa A., Fukunishi Y., Konno H., Kondo S., Yamanaka I., Atagwa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Asito T., Okazaki Y., Golobori T., Bono H., Kasukwa T., Saito R., Atagwa M., Ashburner M., Batalov S., Casvant T., Asito T., Mathi P., Lewis S., Matsuo Y., Nikaido I., Keeole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Ano H., Baldarelli R., Barsh G., Barkai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F., Blake J., Boilt C., Fletcher C., Fujita M., Gariboldi M., Abrowstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Rinnayald M., Rodriguez I., Sakamcto N., Nordone P., Ring B., Rinnayald M., Rodriguez I., Sakamcto N., Saaaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Warshiyaki Y., Kawaji H., Kohtsuki S., Havashiyaki Y., Havashiyaki Y., Havashiyaki Y., Havashiyaki Y., Havashiyaki Y., Havashiyaki Y., Havashiyaki Y., Rawaji H., Kohtsuki S.,
                                                 420
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
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                                       STRAIN=CS7BL/6J; TISSUE=Testis; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hayashizaki Y.; Hayashicaki Y.; Hayashicaki Y.; Meth. Eficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                       EEDVDDEDHDEGFGSEHELSENEEEEEEEDYEDDKDDDISDTFSEPGYENDSVEDLKEV
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                            01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:4932441F15 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
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MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
                                                                                                                                                                                                640 AA.
                                                                                                        TSISSRKRGKRRYFWEYSEOLTPSOOER 448
                                                                                    TSISSRKRGKRRYFWEYSEQLTPSQQER
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                                                                                                                                                                                                QBCDGS_MOUSE PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                               Name=A930001N09Rik;
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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RAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAK 239
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EMBL; AK030092; BAC26779:1; -; mRNA.

Ensembl; RSNUGSGO0000484249; Mus musculus.

MGI; MGI:1924378; A930001N09Rik.

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STRAIN=CSTBL/GJ; TISSUB=Testis;
Shibata K. Tissub=dil076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Komno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Samanoto R., Matsuncto H., Saksguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated Gequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
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92.9%; Score 2195.5; DB 2
Best Local Similarity 92.4%; Pred. No. 7.1e-105;
Matches 415; Conservative 15; Mismatches 18;
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NCBI_TaxID=9606;
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Matches 407;
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EMBL; Ex647768; CAI46039.1; -; mRNA.
Hypothetical protein.
NON TER 408 408
                                                                        OSHYG4 HUMAN PRELIMINARY; PRT; 408 AA.
OSHYG4.
10-MAY-2005 (TEMBLrel. 30, Last sequence update)
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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90.9%; Score 2148; DB 2; Length 408;
Best Local Similarity 99.8%; Pred. No. 1.2e-102;
Matches 407; Conservative 0; Mismatches 1; Indels
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QBGYR3;
01-UNW-2003 (TrEMBLrel. 24, La
01-UNW-2003 (TrEMBLrel. 24, La
01-UNW-2003 (TrEMBLrel. 24, La
Hypothetical protein.
Hymor sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                          The German cDNA Consortium;
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AAAPVCSSKTLQAEVPLSDCVQKASKPTSSTQIMVKTNMYHNEKVNFHVECKDYVKKAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 KINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHATPALPFKETQELLL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930040G19 product:hypothetical protein, full insert sequence.
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii
Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito
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                                                                                                                                                                                            Length 417;
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Li F., Yao K.T.;
Li F., Yao K.T.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, *X174899.
EMBL, *X174899.
Hypothatical protein.
SEQUENCE 417 AA; 46579 MW; 9DBD37B07C14556B CRC64;
                                                                                                                                                                                         90.9%; Score 2148; DB 2; 99.8%; Pred. No. 1.2e-102; ive 0; Mismatches 1;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Q8C8N7;
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                                                                                                                                                                                                                     Similarity
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Fuuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayatsu N., Hirancto K., Hiracka T., Hirozane T., Havia K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Konno H., Kouna M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nakamura M., Nahi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibara K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2010) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO4160; BAC12070.1; -, mRNA.

REBREMD!, ENSWUSGO000048249; Mus musculus.
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kutels S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., A. Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whinning L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hasebi V., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/63; TISSUB=Retina;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matumnoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; TISSUE=Retina;
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NON TER 351 35
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C STRAIN-CSTAINLED SACURANCE.

KX MANIN-CSTAINLED SACURANCE.

KX KAWAIN J. Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

KAWAIN J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

KA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Phkuda S.,

A Arakawa T., Yakunishi Y., Konno H., Adachi J., Phkuda S.,

KA Arakawa T., Saito Y., Osazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

KA Adito T., Matsud H.A., Ashburner M., Batalov S., Gasavant T.,

KA Adito T., Matsud Y., Nikaido I., Pesole G., Quackenbush J.,

KA Chriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

K. Marchionni L., Mashima J., Mazzarelli J., Mombaetts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Nasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

M. Wyashkaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Wyashizaki Y.:

M. Wyashizaki Y.:

M. Washi Y..
                                                                                                  61 SLEDCKDIENLETETDVLDNEDALTSNWEGWDTYCEDLTKYTKLISCDIWGTKEVDYLGL 120
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                                                                                                                                                                                                                                          RAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVNFHVECKDYVKKAK 239
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninoi P., Hayashizaki Y.;
"High-efficiency Full-langh cloning.";
Meth. Bnzymol. 303:19-44(1999).
                   1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
1 MPQPSVSGMDPPFGDAFRSHTFSEQTLMSTDLLANSSDPDFMYELDREMNYQQNPRDNFL
                                                                              61 SLEDCKOIENLESFTDVLDNEGALTSNWEQWDTYCEDLTKYTKLTSCDIWGTKEVDYLGL
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01-0TN-2001 (TrEMBLrel. 17, Last sequence update)
01-0TN-2001 (TrEMBLrel. 17, Last annotation update)
01-0TN-2001 (TrEMBLrel. 17, Last annotation update)
Mus musculus adult retina cDNA, RIKEN full-length enriched library,
clone:A930001N09 product:hypothetical protein, full insert sequence.
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Q9CTQ7;
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DB 2; Length 351; Indels

Score 1704.5; DB 2; Pred. No. 5.9e-80; 9; Mismatches 16;

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Best Local Similarity Matches 325; Conserv

351 AA; 39254 MW; ABA4B36D996AFAAD CRC64;

NON TER SEQUENCE Query Match

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241 VKINPVQQGRPLLSQVHIDAAKENTCYCGAVAKRQERRGVEPHQGRGTPALPFKETQELL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CB; TISSUE=Bursa;
Caddwell R.B., Katezek A.M., Arakawa H., Bezzubov Y., Zaim J.,
Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
Full-length cDNAs from chicken bursal lymphocytes to facilitate
genefunction analysis.";
Genome Biol. 6:R6-R6(2005).
Hypothetical protein.;
Hypothetical protein.

9 CAG31108.1; -; mRNA.
Hypothetical protein.
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Pred. No. 1.3e-26;
6; Mismatches 7; Indels
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAF15001, whole genome shotgun sequence.
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Last annotation update)
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90.1%;
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Q4RRX3;
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STRAIN=C57BL/6J; TISSUB=Retina;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Pukunishi Y., Furuno M.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Sanaki J., Sasaki D., Shibata K., Shibata Y., Shibata C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata X., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y., Shibata Y.,
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                                                                The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002)
                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J; TISSUB=Retina;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                    STRAIN=C57BL/6J; TISSUE=Retina;
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Matches 306; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Tetrandon nigroviridis (Green puffer).

Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi,
Actinopterygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha, Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Local Similarity 24.09
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                                                                NUCLEOTIDE SEQUENCE
STRAIN=PK-1;
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                                   NCBI_TaxID=37296;
                                                                                                                                                               genotypes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 NTCYCGAVAKRQEKKGMEPLQGHATPALP-FKETQELLLSPLPQEGPGSLAAGESSSLSA 321
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Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lauder V., Schachker V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.; "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
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                                                                                                                                                                                                                                                                                                                               27.2%; Score 644; DB 2; Length 600;
34.0%; Pred. No. 3.2e-25;
tive 56; Mismatches 104; Indels 162; Gaps
                                                                                                                                                                                                                       CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                             , Whitehead Institute Centre for Genome Résearch; (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                       600 AA; 66291 MW; B2F28B2F3B27B1C4 CRC64;
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Last annotation update)
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                                                                                                                                     the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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(TrEMBLrel. 16, I
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Matches 166; Conservative
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Q9DUNO;
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SEQUENCE
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Q9DUNO HHV8
ID Q9DUNO;
AC Q9DUNO;
DT 01-MAR-IDT 01-MAR-IDT 01-MAR-IDT O1-MAR-IDT O1-MAR-IDT OFF73.
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MEDLINE=20381179; PubMed=10900044;
MEDLINE=20381179; PubMed=10900044;
MEDLINE=20381179; PubMed=10900044;
MEDLINE=20381179; PubMed=1090004 as S.J.;
Flang Y.J., Deng J.H., Rabkin C., Gaco.J.;
Molear antigen and application in genotyping by PCR-RFLP.";
J. Gen. Virol. 81:2049-2058 (2000).
EMBL; AR192756; AAG0155.1; -1.
GO; GO:0005885; C:cytoskeleton; IEA.
InterPro; IPR002017; Spectrin.
SEQUENCE 976 AA; 112017 MW; ES781E2A509FF70B CRC64;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
NCBI_TaxID=37296;
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Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                     MEDLINE=99445611; PubMed=10515805; DOI=10.1086/315098; Gao S.J., Zhang Y.J., Deng J.H., Rabkin C.S., Flore O., Jenson H.B.; Molecular polymorphism of Kaposi's asrcoma-associated herpesvirus fluman herpevirus 8) latent nuclear antigen: evidence for a large repertoire of viral genotypes and dual infection with different viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74;
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24.0%; Pred. No. 0.074;
tive 56; Mismatches 149; Indels 7
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0911X7 HTV8

10911X9 HTV8

AC 0911X9 F

DT 01-DEC-T

DT 01-DEC-T

DT 01-MAR-7

DE ORP73

OC VITUBES

OC Gammaher

OC Gammaher

OC CAMMAHER
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Spectrin. 131346 MW; 8F63855B45F79109 CRC64;

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InterPro; IPR002017;
SEQUENCE 1129 AA;
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SEQUENCE 26
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89;
                                          MEDLINE=21376412; PubMed=11483733; DOI=10.1128/JVI.75.17.7882-7892.2001; Garber A.C., Shu M.A., Hu J., Renne R.; Bunding and medulation of gene expression by the latency-associated nuclear antigen of Kaposi's sarcoma-associated
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                                                                                                                                                                                                                                               J. Virol. 75:7882-7892(zuu1).

EMBL; AR360120; AAK50002.1; -; Genomic_DNA.
GO; GO:0005856; C:Cytoskeleton; IEA.
InterPro; IPR002017; Spectrin.
SEQUENCE 1003 AA; 115517 MW; C20C43308B01A0A3 CRC64;
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Last annotation update)
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Gammaherpesvirinae; Rhadinovirus.
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AC Q9QR71;
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                                                                                                                                                                                                                                                                                             163 PPPSQOTTPPHSPTTPPPEPPSKSSPDSLAPSTLRSLRKRRLSS------PQ
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                                                                                                                                                                                                                                                                                                                                                                                                209 GPSTLNPICQSPPVSPPRCDFANRSVYPPWATESPIYVGSSSDGDTPPRQPPTSPISIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATPALPF -- KETQELLL -----SPLPQEGPGSLAAGESSSLSASTSVSDSSQKKEEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     269 SSPSEGSWGDDTAMLVLLAEIAEEASKNEKECSENNQAGED---NGDNEISKESQVDKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome sequence and comparative analysis of the model rodent malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Salzberg S.L., Venter J.C., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                              Gaps
                                                              85;
Length 1129;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
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2649 AA; 309810 MW; E7207F344643AC24 CRC64;
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Nature 413:512-19(2002).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
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Last annotation update)
8.1%; Score 191.5; DB 2;
25.0%; Pred. No. 0.12;
iive 52; Mismatches 142;
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EMBL, AABLO100172; EAA18637.1;
InterPro; IPR011591; Botulinum.
ProDom; PD001963; Botulinum; 2.
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Q7RAS7;
01-MAR-2004 (TrEMBLrel. 26, C.
01-MAR-2004 (TrEMBLrel. 26, L.
01-MAR-2004 (TrEMBLrel. 26, L.
Hypotherical protein.
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Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996)

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                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97121480; PubMed-8962146; DOI=10.1073/pnas.93.25.14862; Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D., Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.; Involeotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV9)...;
                                                                                         167 PLPSSFPGKKITSRAAAPVCSSKTLQAEVPLSDCVQKASKPPSSTQIMVKTNMYHNEKVN
                                                                                                                                                                                                                                                                                                                                                     227 PHVECKDYVKKAKVKINPVQQSRPLLSQIHTDAAKENTCYCGAVAKRQEKKGMEPLQGHA
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                      15 DAFRSHTFSE-----OTLMSTDLLANSSDPDFMY------ELDREM-----N
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                                    Indels 169;
   Length 2649;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
ch 8.1%; Score 190.5; DB 2; 1 Similarity 20.6%; Pred. No. 0.36; 93; Conservative 74; Mismatches 116;
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J. Virol. 70:8218-8223(1996).
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8.0%; Score 190; DB 2; Length 1162;
Best Local Similarity 24.2%; Pred. No. 0.15;
Matches 94; Conservative 50; Mismatches 137; Indels 108; Gaps
                                            Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, U52064, AAC55944.1; -; Genomic_DNA.

InterPro; IPR002017; Spectrin.

SEQUENCE 1162 AA; 135213 MW; 1A72CE01C1CB0B1C CRC64;
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Aau73263 Human mbp
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25 5.1.7 Biocceleration Ltd. 27	29 30 11.1me 0.685046 Seconds 3.1 31.5gmmente) 33 31.8milion cell undates/sec 34		410		2443163 45		RESUL AANG TD	XX XX AA AC AA	XX XX		XX XX KW An XXW T-	chance to have a OS	result being printed, AX letribution.		PF V	on Acceptance PR	PR	Motif use XX Internali PA	Native se AX HIV princ PI	Tetrapept DR	Adw46523 Eptide c PT Ar Aaw46483 HIV-1 MO/ PT st Aw87477 HIV-1 mut PT st	Human sem XX Immunisat PS	AE101 ana XX IL-2 deri CC	IL-2 deri CC IL-2 deri CC IL-2 deri CC	3633 Insectici	Cathepsin CC Mammalian CC Synthetic CC	
GenCore version 5.1.7 Copyright (c) 1993 - 2006 Bioccel	OM protein - protein search, using sw model Run on: February 28, 2006, 08:37:25 , Search (Without a	Title: US-10-717-665A-44_COPY_448_449 Perfect score: 10 Sequence: 1 RM 2	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 2443163 seqs, 439378781 residues	er of hits sa seg length:	Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	A_Geneseq_21:* : geneseqp1980s	: geneseqp1990s : geneseqp2000s	geneseqp2001s	6: geneseqp2003as:* 7: geneseqp2003bs:* 8: geneseqp2004s:* 9: geneseqp2005s:*	No. is the number of results predicted	eater than or equal to the score of the srived by analysis of the total score	SUMMARIES	Query	Score	10 100.0 3 2 10 100.0 3 5	10 100.0 4 1 10 100.0 4 2	10 100.0 4 2 10 100.0 4 2	10 100.0 4 2	9 10 100.0 4 2 AAW3//26 10 10 100.0 4 2 AAW46523 11 10 100.0 4 2 AAW87483 12 10 100.0 4 2 AAW87477	10 100.0 4 2	10 100.0 4 2 10 100.0 4 3	10 100.0 4 3	10 100.0	10 100.00 10 100.00 10 100.00 1	

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including a response not associated with inflammation. The peptides also inhibit the ability of macrophages and T-cells to adhere to extracellular matrix components and fibronectin, as well as up-regulated fas receptor expression in T-cells. They can be used to inhibit unwanted immune
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17-JAN-2001; 2001US-00765101.
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RM
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                                                                                                                                                                                                                                                                                                                                                    ABG77780;
                                                                                                                                   Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                        Oligopeptide and polypeptide compsns. - based on the amino acid sequence of an immunogen and used for modulating the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Internalisation signal; core; modulation; receptor; transport; ligand; cytoplasmic tail; endocytosis.
                                                                                        Motif useful in tolerization alone or in association with epitopes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                           Autoantigen; MBP; myelin basic protein; transplantation antigen;
myasthenia gravis; myasthenics; Transplantation antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100.0%; Score 10; DB 1; Length 4; Similarity 100.0%; Pred. No. 2e+06; 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                     (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR41636 standard; peptide; 4 AA.
           AAP91627 standard; protein; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page; 7pp; English.
                                                                                                                                                                                                                                        88EP-00307608
                                                                                                                                                                                                                                                               87US-00086694
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                                                          (revised)
(first entry)
                                                                                                                                                                                                                                                                                                             Zamvil S;
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                                                                                                        proteolipid protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                               17-AUG-1987;
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10-MAR-1994
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                                                                                                                                                                                                                 22-FEB-1989.
                                                                                                                                                                                                                                                                                                               Steinman L,
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09-JUL-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                   Synthetic.
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                                  AAP91627;
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AAP91627
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Claim 52; Page 11; 116pp; English.

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The sequences given in AAA41636-57 represent the cores of internalisation signals which were used in the method of the invention for modulating receptor mediated transport of a ligand into a cell. These sequences are derived from the cytoplasmic tails of surface receptors. These amino acid internalisation signals have a tight turn structure. The introduction of one of these sequences into a receptor within a cell, modulates the transport of ligand into a cell having a surface receptor reactive with that ligand. This modulation can cause an increase or a decrease in endocytosis, depending on the choice of internalisation signal. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide(s) and analogues based on amyloid precursor protein - used for promoting neuronal growth in conditions involving damage to neurons or in treating Alzheimer's Disease etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Native secreted amyloid precursor protein (APP) antagonistic peptide.
                                                                                                                                                                          - by
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                                                                                                                                                                          Modulating receptor mediated transport of ligand into cell introducing heterologous internalisation signal into cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amyloid precursor protein- antagonist; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 100.0%; Score 10; DB 2; Length 4; Local Similarity 100.0%; Pred. No. 2e+06; hes 2; Conservative 0; Mismatches 0; Indels
                                                                                                                  Kuhn LA;
                                                                                                                Trowbridge IS, Collawn JF, Tainer JA,
                                                                    (SALK ) SALK INST BIOLOGICAL STUDIES (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR54662 standard; peptide; 4 AA.
                                                                                                                                                                                                                       Claim 16; Page 49; 60pp; English.
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             93WO-US001669.
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(first entry)
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                                                                                                                                              WPI; 1993-303496/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuron growth.
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             01-MAR-1993;
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                                         03-MAR-1992;
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29-NOV-1994
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AAR54662
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An antigenic conjugate, useful as a vaccine for AIDS, has the formula (SPNE)n-(OMPC), where SPNE is a selected principal neutralisation epitope of HIV, which is one of 16 specified polypeptides (including the present sequence) or their fragments containing at least 5 amino acids; OMPC is purifited outer membrane proteosome of Neisseria (pref. N. meninglitidis); and n is 1-200, indicating the number of SPNE moieties covalently linked to the OMPC. The conjugates may be substituted by anions, and conjugation may be via a bigeneric spacer. The SPNE polypeptides bind an HIV broadly neutralising monoclonal antibody (559 antibody) that binds gpl20 and also inhibits the binding of HIV to CD4. They were originally identified in the bitope polypeptides accessible to the antibody. The libraries were ALPHA and EPSILON described in AAR83295 and AAR83299 respectively. The sequences of these polypeptides were deduced from their corresponding DNA sequence.
                                                                                                                                                                                                ö
                            This sequence corresponds to AA 330-333 of amyloid precursor protein. This peptide, which partially overlaps the C-terminal side of thet acti sequence RERMS (AAR54661), acts to antagonize the activity of secreted APP (695 AA). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antigenic conjugate useful as vaccine for AIDS - comprising HIV principal neutralisation epitope covalently linked to outer membrane proteosome of Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV principal neutralisation epitope binding to 559 antibody.
                                                                                                                                                        100.0%; Score 10; DB 2; Length 4; 100.0%; Pred. No. 2e+06; cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keller PM;
                                                                                                                                                                                                                                                                                                                                                                   AAR93665 standard; peptide; 4 AA.
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                                                                                                                                                                                                  2; Conservative
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                                                                                                                                                              Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                          Sequence 4 AA;
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AAW77469 standard; peptide; 4 AA.
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                                                               AAW77469;
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Matches
                    RESULT 8
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/note= "Z-Phe-psi[PO2CH2]-Ala, where Z is benzyloxy-carbonyl and -psi[PO2CH2]- indicates replacement of the peptide linkage -CONH- between Phe and Ala by the group PO2CH2-"
                                                                                                                                                                                            Zinc endopeptidase; EC.3.4.24-15; selective inhibitor; analgesic; pain; hypothermia; arterial hypertension; cancer; Alzheimer's disease; phosphinic acid; pseudopeptide linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide derivs. contg. phosphonic acid gp. replacing an amide bond are highly specific inhibitors of endo:peptidase 24-15, for treating hypothermia, hypertension, cancer, Alzheimer's disease etc.
Gaps
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                                                                                                                                                                        retrapeptide useful as zinc endopeptidase 24-15 inhibitor.
 0; Indels
  Mismatches
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                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                        AAW86792 standard; peptide; 4 AA.
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Best Local Similarity 100.
Matches 2; Conservative
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   Conservative
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Modified-site
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      Matches
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                                                                                                                                                                                                                                                                                                                                                                          1. .2
/note= "Z-Phe-psi[PO2CH2]-Gly, where Z is benzyloxy-carbonyl and -psi[PO2CH2]- indicates replacement of the peptide linkage -CONH- between Phe and Gly by the group PO2CH2-"
                                                                                                 Zinc endopeptidase; EC.3.4.24-15; selective inhibitor; analgesic; pain; hypothermia; arterial hypertension; cancer; Alzheimer's disease; phosphinic acid; pseudopeptide linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptide derivs. contg. phosphonic acid gp. replacing an amide bond are highly specific inhibitors of endo:peptidase 24-15, for treating hypothermia, hypertension, cancer, Alzheimer's disease etc.
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                                                Tetrapeptide useful as zinc endopeptidase 24-15 inhibitor.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-356059/36.
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Modified-site
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06-JUL-1999
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ID AAW3
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AAW37726;

Synthetic.

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peptides AAW46520-53 contain protease binding sites. They are used to produce novel reagents whose fluorescence increases in the presence of produce novel reagents whose fluorescence increases in the presence of particular proteases. These fluorescent signal at a visible wavelength when they are digested by a protease. The fluorogenic indicators have the general formula: F1-C1-P-C2-F2 | (S1)n (S2)k where: P is a peptide containing a protease binding site, e.g. AAW46520-33. F1 and F2 are containing a protease binding site, e.g. AAW46520-33. F1 and F2 are contornation-determining regions that introduce a bend into the composition which positions the fluorophores adjacent to each other with a separation of less than 100 Angstrom. When n is 1, S1 is joined to the terminal alpha -amino group of C1 by a peptide bond, and when k is 1, S2 is joined to the terminal carboxy group of C2 by a peptide bond. The procease indicators are used for detecting protease activity in a biological sample. The sample is contacted with the indicator and any change in fluorescence is detected, an increase in fluorescence indicating protease activity
                                                                                                                                                                                                                                      Fluorogenic substrates for protease determination - having two closely spaced fluorophores flanking protease binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus-1; HIV-1; protease; provirus; L-2 cell; mutation; Nef protein; immunogen; apoptosis; treatment; hybridisation; cell lysis; chemotherapeutic; toxin; HIV infection; MO/LAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 10; DB 2; Length 4; 100.0%; Pred. No. 2e+06; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                        Disclosure; Col 4; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus 1.
                                                           94US-00331383
                    95US-00549008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                Packard BS, Komoriya A;
                                                                                                       (ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                            WPI; 1998-158345/14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4 AA;
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                    27-OCT-1995;
                                                              28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9844945-A1
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11-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying DNA encoding inducible or suppressible cytochrome P450 - by screening for drugs which reduce the catabolism of retinoic acid, useful in cancer chemotherapy and the treatment of acne and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protease binding site; protease; protease indicator; fluorescent signal; detection; protease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is a degenerate peptide from which the PCR primer used in the amplification process is derived. The PCR involves the inducible cytochrome P450 gene which produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. A form of cytochrome P450 is P450RAI which specifically metabolises a derivative of retinoic acid (RA). It is highly induced by RA in cell lines and tissues. This allows for the development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                   Degenerate peptide; PCR; amplification; cytochrome P450 gene; oxidative metabolism; P450RAI; retinoic acid; RA; promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h Similarity 100.0%; Score 10; DB 2; Length 4; Similarity 100.0%; Pred. No. 2e+06; 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide containing a protease binding site.
                                                                                                         Cytochrome P450 degenerate primer 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 61; 113pp; English.
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96US-00724466.
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                                                              (first entry)
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petkovich PM;
                                                                                                                                                                                                                                                               WO9749832-A2
                                                                                                                                                                                                                                                                                                                                                    23-JUN-1997;
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                                                              07-JUL-1998
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Gaps

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98WO-US006690. 97US-0043047P

03-APR-1998; 04-APR-1997;

JS5714342-A

AAW46523;

RESULT 10

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03-FEB-1998

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15-0CT-1998

97US-0043047P

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Human immunodeficiency virus-1; HIV-1; protease; provirus; L-2 cell;
mutation; Nef protein; immunogen; apoptosis; treatment; hybridisation;
cell lysis; chemotherapeutic; toxin; HIV infection.
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           HIV-1 mutant env gp120 amino acid fragment in L-2 cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "encoded by GAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        AAW87477 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus 1.
                                                                                        Example 1; Fig 1; 66pp; English
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      (IMMU-) IMMUNE RESPONSE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                     WPI; 1998-568304/48.
                                            N-PSDB; AAV71866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                       Sequence 4 AA;
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11-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                        AAW87477;
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AAW87477
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the defective human immunodeficiency virus-1 (HIV-1) provirus in L-2 cells. They represent the portions of pol protease (prot.), vpr, env cells. They represent the portions of pol protease (prot.), vpr, env cells. They represent the portions of pol protease (prot.), vpr, env captured as compared to wild-type HIV-1 in LAI or MO/LAI cells. The invention relates to mutated to DNA, proteins or fragments of defective HIV-1 provirus in L-2 cell line. The mutations result in non-infections HIV-1 particles. Inactive, creducing or preventing are used as immunogens, particularly for truncated protein fragments are used as immunogens, particularly for cruncated protein fragments are used as immunogens, particularly for cubjects, specifically those with HIV-1 infection, both for prevention and treatment. Pragments of nef gene and fragments encoding specific and treatment. Pragments of nef gene and fragments encoding specific detection of mutated genes in (lysed) cells or body fluids, while the corresponding mutant proteins are detected in immunoassays using corresponding mutant proteins are detected in immunoassays using corresponding attached to a radiciscope, chemotherapeutic agent or toxin, can be used to reduce the severity of HIV infections. (Updated on 17-OCT-can be used to reduce the severity of HIV infections.
                                                                                                                                                                                                                                                                                                         New nucleic acid encoding mutant or truncated forms of human immune deficiency virus proteins - used to generate non-infectious particles useful as therapeutic or prophylactic immunogens, also for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAW87475 to AAW87463 represent mutant amino acid sequences
the defective human immunodeficiency virus-1 (HIV-1) provirus in 1.-?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1; 66pp; English
                                                                      (IMMU-) IMMUNE RESPONSE CORP.
                                                                                                                                                                                                                    WPI; 1998-568304/48
                                                                                                                                                                                                                                                     N-PSDB; AAV71860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4 AA;
04-APR-1997;
       AAW87481 to AAW87486 represent human immunodeficiency virus-1 (HIV-1) caid sequences in Mo/LAI cells that were used for comparing the mutant amino caid sequences of the defective HIV provirus in L-2 cells. AAV1858 to AAV1858 represent the portions of pol protease (proc.), vpr. env (gpl20 and gp41), and nef gene regions that were mutated as compared to wild-type HIV-1 in LAI or MO/LAI cells. The invention relates to mutated DNA, proteins or fragments of defective HIV-1 provirus in L-2 cell line. The proteins result in non-infectious HIV-1 particles. Inactive, protease-containing at least one of Nef truncated protein fragments are used as immunogens, particularly for reducing or protein grapposes in HIV-1 sero-negative or -positive subjects, specifically those with HIV-1 sero-negative or -positive subjects, specifically those with HIV-1 infection, both for prevention and treatment. Fragments of nef gene and fragments encoding specific mutant of metated genes in (lysed) cells or body fluids, while the corresponding mutant proteins are detected in immunoassays using carticonally attached to a radioisotope, chemotherapeutic agent or toxin, can be used to reduce the severity of HIV infections. (Updated on 17-OCT-can be used to reduce the severity of HIV infections. (Updated on 17-OCT-
                                                                                                                                                                                                                                                                                              New nucleic acid encoding mutant or truncated forms of human immune deficiency virus proteins - used to generate non-infectious particles useful as therapeutic or prophylactic immunogens, also for diagnosis.
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Query Match
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 1 RM 2 ٣ S ઠે 셤 .; 0 Gaps ö

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Gaps ö

WO9845322-A2

15-0CT-1998.

Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-b; presentiln II; presentiln II; cellular tumour antigen; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-I; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A; high mobility group protein-C; neuroendocrine specific protein A. Human semaphorin III mutant protein fragment 16. AAY21283 standard; protein; 4 AA. 22-JUL-1999 (first entry) Homo sapiens AAY21283; RESULT 13

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but which may be used with advantage for tolerisation by itself or in conjunction with other epitope sequences from the present invention. The present invention describes a polypeptide comprising a human myelin basic protein (PMBP) fragment including P89-101 of PMBP, excluding native hMBP. The term P89-101 is not defined but may be intended to mean amino acids 89-101 of hMBP. The polypeptide can be used for tolerising a mammalian host immune system comprising B and T cells to an immunogen of interest, wherein said immunogen is restricted by a transplantation antigen of said host. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-
                                                                                                                                                                                                                                                                                                        sequence represents an immunisation motif normally excluded,
                                                                                                                                                                                          Polypeptide comprising human myelin basic protein fragment - useful as immuno modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalian Ii key peptide; mammalian invariant chain protein; allergy;
immune response; MHC class II; antigenic; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mammalian invariant chain protein (Ii) key peptide(s) - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 10; DB 2; Length 4; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AE101 analogue effector compound SEQ ID NO:26.
                                                                (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW47950 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Amidated"
                                                                                                                                                                                                                                                                 Disclosure; Page 8; 8pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu M;
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87US-00086694
                    88EP-00307608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams S,
                                                                                                         Steinman L, Zamvil S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-076917/07.
                                                                                                                                                     WPI; 1998-034664/04
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-1997;
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17-AUG-1987;
                    17-AUG-1988;
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##X#X#X#X##X##X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related disease, especially cancer and a wide range of neurodegenerative disorders [e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, Indianated by a locationis, a locationic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated protein 2 (MAP2), neurofilament-I, neurofilament-M, neurofilament-P, presentiin I, presentiin II, glial fibrillary acidic protein (GRAP), the cellular tumour antigen ps; Herell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A
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                                                                                                                                                                                                                                                                                                      Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 10; DB 2; Length 4; 100.0%; Pred. No. 2e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                 Burbach JPH;
                                                                                                         (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
(UYRO-) UNIV ROFTERDAM ERASMUS.
(UYUT-) RIJKSUNIV UTRECHT.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 16; 258pp; English.
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                                                                                                                                                                                                 Van Leeuwen FW, Grosveld FG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97EP-00106788.
                       98WO-IB000705
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                                                                                                                                                                                                                                          WPI; 1998-609901/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                 N-PSDB; AAX75767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4 AA;
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                       02-APR-1998;
                                                                  10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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08-JUL-1998
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Matches
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Gaps

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The present sequence represents an AE101 analogue effector compound used in the present invention describes a mammalian invariant chain protein (Ii) key peptide of sequence LRWKLPKPEKVSKWR and modifications with the exclusion of peptide YRWLDFPEPKPVSKWR. MHC class II molecules are synthesised in the endoplasmic reticulum with their antigenic peptide sites blocked by the invariant chain protein (Ii). The products and method can be used for the modulation of an immune response for therapeutic or diagnostic purposes. The enhancement of immunity can be used in the treatment of e.g. malignant or allergic disease. The immunosuppression can be used for the treatment of autoimmune disease, e.g. rheumatoid arthritis, multiple sclerosis, diabetes mellitus, lupus erythematosus, and psoriasis or allograft rejection modulation of immune response, e.g. for treating malignant, allergic autoimmune disease or allograft rejection. Example 1; Page 27; 149pp; English.

Sequence 4 AA;

ö 0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 2; Conservative 0; Mismatches 0; Indels

1 RM 2 | | 2 RM 3

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Search completed: February 28, 2006, 08:45:08 Job time : 2.68505 secs

75, Appl 77, Appl 78, Appl 173, App 46, Appl 9, Appli 4, Appli 90, Appli

Sequence Sequence Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

Sequence

OM protein

Run on:

Sequence:

Title: Perfect

Searched:

Database

Result

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Sequence
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
ITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 10; DB 1; Length 3; 100.0%; Pred. No. 4.6e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTK:.

ZIP: 03911
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
'OPERATING SYSTEM: PatentIn Release #1.0, Version #1.25
'OPERATION DATA:
'OR/968,676
US-08-350-260A-413
US-08-818-253-58
US-08-094-173-46
US-09-020-880-75
US-09-020-880-77
US-09-120-880-77
US-09-131-906A-9
US-09-191-906A-9
US-09-101-649-13
US-08-310-9113-90
US-08-818-111-91
US-08-818-111-91
US-08-818-111-91
US-08-818-111-91
US-09-101-544-75
US-09-101-544-77
US-09-101-544-77
US-09-101-544-77
US-09-101-544-77
US-09-101-544-77
US-09-101-544-77
                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
TELEPAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C. STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                          Sequence 27, Application US/08968676
Patent No. 5919639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35,505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 2; Conserv
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                                                                                                                 (without alignments)
960.804 Million cell updates/sec
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                                                                                                  February 28, 2006, 08:53:26; Search time 0.172097 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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                GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-055-075C-18
US-09-919-113-18
US-09-919-124-16
US-09-919-124-18
US-09-681-201-2
US-09-2661-894A-26
US-09-763-233A-2
US-09-763-233A-3
US-09-763-293A-31
US-09-763-293A-31
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S-09-191-906A-2
S-09-101-649-12
S-09-055-075C-16
S-09-055-075C-18
                                                                                                                                                                                                                                                                                 Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -08-504-265B-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-894-922A-2
US-08-968-676-25
                                                                                                                                                    US-10-717-665A-44_COPY_448_449
                                                                                                                                                                                                                                                        572060 seqs, 82675679 residues
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                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents AA:
                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                           Copyright
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MOLECULE TYPE: peptide
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          ; MOLECULE ...
US-08-331-383-4
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Sequence 4, Application US/08311383

Sequence 4, Application US/08311383

Patent No. 5605809

GENERAL INFORMATION:

APPLICANT: Romoriya, Akira

APPLICANT: Packard, Beverly S.

TITLE OF INVENTION: Compositions for the Detection of

TITLE OF INVENTION: Thereof

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend Khourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

STREET: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                          Sequence 27, Application US/09261894A

Sequence 27, Application US/09261894A

Patent No. 6815382

GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT E.

APPLICANT: ADAMS, SHARLENE

APPLICANT: ADAMS, SHARLENE

APPLICANT: XU, MINZHEN

TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION

TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN PRESENTATION

TITLE OF INVENTION: 1999-03-03

CURRENT APPLICATION NUMBER: US/09/261,894A

CURRENT FILING DATE: 1999-03-03

NUMBER OF SEQ ID NOS: 167

SOFTWARE: PATENTIN VET: 3.2

SEQ ID NO 27

LENGTH: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic ; OTHER INFORMATION: peptide US-09-261-894A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3;
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ZIP: 94105

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,383
FILING DATE: 28-0CT-1994
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 10; DB 2; I
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TALLANDIAN MARE 100, KATER B.
REGISTRATION NUMBER: 29,684
REFRENCE/DOCKET NUMBER: 16865
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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us-08-549-008-4
; Sequence 4, Application US/08549008
; Patent No. 5714342.
; GENERAL INFORMATION:
GENERAL INFORMATION:
; APPLICANT: Romoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
; TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
; ONRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; COURTY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-2-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Ouery Match
Best Local Similarity 100.0%; Score 10; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTED 13934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/549,008
FILING DATE: 27-OCT-1995
FLING APPLICATION 135
PRICK APPLICATION NUMBER: US/08/331,383
ATTOMEN/AGENT INFORMATION:
ATTOMEN/AGENT INFORMATION:
ATTOMEN/AGENT INFORMATION:
ATTOMEN/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        016865-000110US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REPERENCE/DOCKET NUMBER: 0168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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APPLICANT: Wachman, Ronald J
APPLICANT: Gareide, Christopher S
APPLICANT: Gareide, Christopher S
APPLICANT: Tobe, Stephen S
TITLE OF INVENTION: Mimetic Insect Allatostatin Analogs for Insect Control
FILE REFERENCE: P.C. 0047.99-Ronald J. Nachman et al.
CURRENT APPLICATION NUMBER: US/09/191,906A
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Andersen, Thomas T.
Bizios, Rena
TITLE OF INVENTION: Peptides for
Altering Osteoblast Adhesion
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Healin & Rothenberg, P.C.
STREET: 5 Columbia Circle
CITY: Albany
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
  DE 197 01 141.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09191906A Patent No. 6207643 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09101649
Patent No. 6262017
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          °,
                 FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G-
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 026/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                31,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Diploptera punctata
US-09-191-906A-2
                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                4 amino acide
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RM 2
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US-09-191-906A-2
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                                                                                                                                                                   TELEFAX:
TELEX: 9
                                                                                                                                                                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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APPLICANT: Mueller, Rolf
APPLICANT: Sedlacek, Hans-Harald
APPLICANT: Sedlacek, Hans-Harald
TITLE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
TITLE OF INVENTION: ACTIVE SUBSTANCES WHICH CAN BE ACTIVATED BY PROTEASES, AND
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
TUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
STREET: P.O. BOX 999
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITX: "C. STATE: D.C. C. STATE: D.C. COUNTRY: USA ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: Patentin Release #1.0, Version #1.30 SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: D.C. CURRENT APPLICATION NUMBER: US/09/008,308 PTI.NG DATE: 16-JAN-1998
                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3000 K Street, N.W., Suite 500 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0558
                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23, Application US/09008308 Patent No. 6080575 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                      03911
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                                                                                                                                                               COUNTRY:
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Sequence 16, Application US/09919124

Sequence 16, Application US/09919124

Sequence 16, Application US/09919124

GENERAL INFORMATION:

APPLICANT LUKING Ronald B.

TITLE OF INVENTION: No. 6557296-Infectious, Protease Defective HIV Particles and

TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor

FILE REFERENCE: PIM 4867

CURRENT APPLICATION NUMBER: US/09/919,124

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/043,047
                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Luftig, Ronald B.
TITLE OF INVENTION: No. 6328976-Infectious, Protease Defective HIV Particles and
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor
CURRENT APPLICATION NUMBER: US/09/055,075C
CURRENT FILING DATE: 1998-04-03
PRIOR PILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Description of Artificial Sequence: Modified mouse; OTHER INFORMATION: Ii key peptide US-09-396-813-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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; Sequence 3, Application US/09396813
; Patent No. 6432409
; GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E.
APPLICANT: Xu, Minchen
; APPLICANT: Xu, Minchen
; TITLE OF INVENTION: HYBRID PEPTIDES MODULATE THE IMMUNE RESPONSE
; FILE REPERENCE: REHAZOO7
; CURRENT APPLICATION NUMBER: US/09/396,813
; CURRENT FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

100.0%; Score 10; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;

Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        , OCGANISM: Human immunodeficiency virus type 1 US-09-055-075C-18
US-09-055-075C-18
; Sequence 18, Application US/09055075C
; Patent No. 6328976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-919-124-16
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Sequence 16, Application US/09055075C

Sequence 16, Application US/09055075C

Sequence 16, Application US/09055075C

SENERAL INFORMATION:

APPLICANT: Luftig, Ronald B.

TITLE OF INVENTION: No. 6328976-Infectious, Protease Defective HIV Particles and TITLE OF INVENTION: No. 6328976-Infectious, Protease Defective HIV Particles and FILE REFERENCE: P-IM 3074

CURRENT APPLICATION NUMBER: US/09/055,075C

CURRENT FILING DATE: 1998-04-03

PRIOR FILING DATE: 1997-04-04

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16
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                                                                                                          COMPUTER: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: DISKETE, 486
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Word DATA: Word DATA: APPLICATION DATA: US/09/101,649
FILING DATE: 14-Jul-1998
PRIOR APPLICATION NUMBER: 60/010,026
FILING DATE: 16-JAN-1996
APPLICATION NUMBER: 60/029,189
FILING DATE: 31-OCT-1996
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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hansen, Philip E.
REGISTRATION NUMBER: 32700
REGISTRATION NUMBER: 0094.026BWO
TELECOMMUNICATION INPORMATION:
TELEPHONE: (518) 452-5600
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-055-075C-16
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SEQUENCE DESCRIPTION: SEQ ID NO: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                       ZIP: 12203
COMPUTER READABLE FORM:
                   STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RM 2
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Sequence 23, Application US/09256237
Patent No. 6670147
GENERAL INFORMATION:
APPLICANT: Heidemann, Hans H.
Mueller, Rolf
Sedlacek, Hans-Harald
IIILE OF INVENTION: NUCLEIC ACID CONSTRUCT FOR EXPRESSING
ACTIVE SUBSTANTES WHICH CAN BE ACTIVATED BY PROTEASES, AND
PREPARATION AND USE
                           Gaps
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                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DAIA:
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  Pred. No. 4.6e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 026083/0189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/008,308
FILING DATE: 16-JAN-1998
APPLICATION NUMBER: DE 197 01 141.1
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/256,237
FILING DATE: 24-Feb-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 28, 2006, 08:56:08 Job time : 1.4221 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 904136
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                         2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 2; Conserv
  Best Local Similarity
Matches 2; Conserv
                                                                   1 RM 2
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US-09-256-237-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANTION:
APPLICANT: Luftig, Ronald B.
APPLICANT: Luftig, Ronald B.
TITLE OF INVENTION: No. 6557296-Infectious, Protease Defective HIV Particles and TITLE OF INVENTION: No. 657296-Infectious, Protease Defective HIV Particles and TITLE OF INVENTION: Nucleic Acid Molecules Encoding Therefor FILE REFERENCE: P-IM 4867
CURRENT APPLICATION NUMBER: US/09/919,124
CURRENT PILING DATE: 1001-07-30
PRIOR PILING DATE: 1001-04-04
PRIOR PILING DATE: 1090-04-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
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Patent No. 6664371
GENERAL INFORMATION:
APPLICANT: Nachman, Ronald J
APPLICANT: Garside, Christopher S
APPLICANT: Tobe, Stephen S
TITLE OF INVENTION: Mimetic Insect Allatostatin Analogs for Insect Control FILE REFERENCE: P.C. 0047.99-Ronald J. Nachman et al.
CURRENT APPLICATION NUMBER: US/09/680,201
CURRENT FILING DATE: 2001-01-19
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                                                                                                                                                                                                                                                    Length 4;
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                                                                                                                                                                                                                                                                                           Indels
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Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                  LENGTH: 4

TYPE: PRT

GRANICAN Human immunodeficiency virus type 1
US-09-919-124-16
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US-09-919-124-18
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                         09/055,075
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SOTTWARE: Patentin Ver. 2.1
SEQ ID NO 2
1, ENV.....
PRIOR FILING DATE: 1997-04-04
PRIOR APPLICATION NUMBER: US 09,
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Diploptera punctata
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Length 4;

DB 2;

100.0%; Score 10;

Query Match

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79, Appl
35, Appl
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US-09-192-854-77
US-09-192-854-108
US-09-751-854-108
US-09-751-1008-46
US-09-968-561A-73
US-09-968-561A-91
US-09-968-561A-127
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US-09-968-561A-217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: FARTELL, Kevin M
REGISTRATION NUMBER: 35,505
REPERENCE/DOCKET NUMBER: REH-9601
TELECOMMUNICATION INFORMATION:
TELEFHONE: (207) 363-0558
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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110, Appl
26, Appl
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2, Appli
3, Appli
8, Appli
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1433.071 Million cell updates/sec
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                                                                                             February 28, 2006, 08:54:36; Search time 0.583124 Seconds
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Sequence 26,
Sequence 48,
Sequence 3, A
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Sequence 48, A
Sequence 3, Al
Sequence 8, Al
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-919-124-18
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US-10-197-000-3
US-10-197-000-3
US-10-197-000-3
US-10-197-2
US-10-197-2
US-10-245-871-8
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US-10-245-871-801
US-10-253-286-8
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US-09-873-459A-30
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Database

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US-09-910-124-18

US-09-910-124-18

US-09-910-124-18

Sequence 18, Application US/09919124

Sequence 18, Application US/09919124

Sequence 18, Application US/09919124

Sequence 18, Application US/09/0919134

GENERAL INFORMATION:

TITLE OF INVENTION: No. US20020061313A1-Infectious, Protease Defective HIV Particles FILE REFERENCE: P.IM 4667

TITLE OF INVENTION: Number: US/09/919,124

CURRENT FILING DATE: 2001-07-30

PRIOR PLICATION NUMBER: 05/043,047

PRIOR PLICATION NUMBER: 05/043,047

PRIOR PLING DATE: 1997-04-04

PRIOR PLING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 48

SEQ ID NO 18

SEQ ID NO 18
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Best Local Similarity 100.0%; Score 10; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
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US-09-98-491-10
i Sequence 10, Application US/09988491
j Publication No. US20030166529A1
j GENERAL INPORMATION:
GENERAL INPORMATION:
j APPLICANT: Mileusnic, Radmilla
APPLICANT: Mileusnic, Radmilla
TITLE OF INVENTION: Polypeptides and their Uses
TITLE OF INVENTION: Polypeptides and their Uses
CURRENT FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR PLING DATE: 2001-04-18
PRIOR PLING DATE: 2001-04-18
PRIOR PLING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
TENDOR 10 NO 10
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100.0%; Pred. No. 1.7e+06;
tive 0; Mismatches 0;
          100.0%; Score 10; DB 3; 100.0%; Pred. No. 1.7e+06; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 4-mer polypeptide US-09-998-491-10
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ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity 100.
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Best Local Similarity
Matches 2; Conserv
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; Sequence 16, Application US/09919124
; Patent No. US20200061313A1
; Patent No. US20200061313A1
; GRERRAL INFORMATION:
   APPLICANT: Luftig, Ronald B.
   TITLE OF INVENTION: No. US2020061313A1-Infectious, Protease Defective HIV Particles
   TITLE OF INVENTION: No. US20200161313A1-Infectious, Protease Defective HIV Particles
   TITLE OF INVENTION: NO. US20200161313A1-Infectious, Protease Defective HIV Particles
   TITLE OF INVENTION: NO. US20200161313A1-Infectious, Protease Defective HIV Particles
   TITLE OF INVENTION: NO. US20200107-30
   PRIOR APPLICATION NUMBER: US 09/095,075
   PRIOR APPLICATION NUMBER: US 09/055,075
   PRIOR FILING DATE: 1998-04-03
   NUMBER OF SEQ ID NOS: 48
   SEQ ID NO 16
   LENGTH: 4
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                                                                                                   Sequence 31, Application US/08484409

Publication No. US20020076412A1

GENERAL INFORMATION:
APPLICANT: Steinman, Lawrence
APPLICANT: Zamvil, Scott
TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIF: 98104-77092

ZIF: 98104-77092

COMPUTER ENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,409
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 690068.409C1
REGISTRATION NUMBER: 690068.409C1
TELEPHONE: (206) 622-4900
TELEFAK: (206) 622-4900
TELEFAK: (206) 622-6331
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
FRACTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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Gaps

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Sequence 86, Application US/10163198

Sequence 86, Application US/10163198

Publication No. US20030126645A1

GENERAL INFORMATION:

APPLICANT: Rebecca E. Cahon;

APPLICANT: Bimer P. Heppard

APPLICANT: Blaner P. Heppard

APPLICANT: Blaner P. Heppard

APPLICANT: Blaner P. Heppard

APPLICANT: Blaner P. Heppard

TITLE OF INVERTION: Alteration Of Embryo/Endosperm Size During Seed Development

TITLE OF INVERTION: AUGUST NABER: 60/295,921

FRIOR APPLICATION NUMBER: 60/295,921

PRIOR FILING DATE: 2001-06-05

PRIOR FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 111

SOFTWARE: Microsoft Office 97

LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Description of Artificial Sequence: Modified mouse; OTHER INFORMATION: Ii key peptide
US-10-197-000-3
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3. Application US/10197000
Publication No. US20030091582A1
GENERAL INFORMATION:
APPLICANT: Humphreys, Robert E.
APPLICANT: Adams, Sharlene
TITLE OF INVENTION: HYBRID PEPTIDES MODULATE THE IMMUNE RESPONSE
FILE REFERENCE: REALO?
CURRENT APPLICATION WUMBER: US/10/197,000
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 4
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100.0%; Score 10; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                         Length 4;
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                                                                                                                                                                       100.0%; Score 10; DB 4; I 100.0%; Pred. No. 1.7e+06;
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                                                                                                     ; OTHER INFORMATION: LRMS Insert
US-10-032-717-48
                                        TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
PEATURE:
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SEQ ID NO 48
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                                                                   Sequence 26, Application US/09261894
Publication No. US20030207324A1
GENERAL INFORMATION:
APPLICANT: Home
APPLICANT: Adams, Sharlene
APPLICANT: Xu, Minzhen
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
NUMBER OF SEQUENCES: 165
CORRESPONDENCE ADDRESS:
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APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sian
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Prote
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN Release #1.0, Version #1.25
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PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                           ADDRESSEE: Kevin M. Farrell, P.C. STREET: P.O. Box 999
CITY: York Harbor
STATE: MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09/261,894
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Publication No. US20020151709A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Farrell, Kevin M
REGISTRATION NUMBER: 35.505
REFRENCE/DOCKET NUMBER: REH-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (207) 363-0528
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09//
FILING DATE: March 3, 1999
CLASSIFICATION:
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1 Sequence 8, Application US/10245871

2 Sequence 8, Application No. US20030235594A1

3 Publication No. US20030235594A1

GENERAL INFORMATION:

3 APPLICANT: HUMPHREYS, ROBERT

APPLICANT: WINZHEN

TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

FILE REPERENCE: REH-2013

CURRENT FILING DATE: 2003-01-09

PRIOR APPLICATION NUMBER: 10/197,000

PRIOR PILING DATE: 2003-07-17

PRIOR PILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARE: PALENTIN VEY. 2.1

SEQ ID NO 8

LENGTH: 4

LENGTH: 4
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| ARPLICANT: HUMPHREYS, ROBERT
| APPLICANT: HUMPHREYS, ROBERT
| APPLICANT: HUMPHREYS, ROBERT
| APPLICANT: WU MINZHEN
| TITLE OF INVENTION: Likey/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| TITLE OF INVENTION: Likey/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| TITLE OF INVENTION: Likey/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| CURRENT FILING DATE: 2003-01-09
| CURRENT FILING DATE: 2002-07-17
| PRIOR PILING DATE: 2002-07-17
| PRIOR PILING DATE: 1999-09-14
| NUMBER OF SEQ ID NOS: 905
| SOFTWARE: PALENTIN VET: 2.1
| SEG ID NO 3
| LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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1larity 100.0%; Pred. No. 1.7e+06;
Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/10245871; Publication No. US20030235594A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Show and the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
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Sequence 2, Application US/10385317
Sequence 2, Application US/20030161857A1
GENERAL INFORMATION:
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GARBIGANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                        Length 4;
                                                                                                                                                          0; Indels
                                                                             100.0%; Score 10; DB 4; L 100.0%; Pred. No. 1.7e+06;
                                                                                                                                                                  0; Mismatches
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Sequence 48, Application US/10414637
Publication No. US20030177528A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Micholas B. Duck
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT (CRANISM: Diploptera punctata US-10-385-317-2
                                                                                         Query Match
Best Local Similarity 100.
Matches 2; Conservative
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3 RM 4
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US-10-659-509-2

US-10-659-509-2

§ Sequence 2, Application US/10659509

§ Publication No. US20040039159A1

§ GENERAL INFORMATION:

§ APPLICANT: Nachman, Ronald J

§ APPLICANT: Tobe, Stephen S

§ TITLE OF INVENTION: Mimetic Insect Allatostatin Analogs for Insect Control

§ TITLE OF INVENTION: Wimber: US/10/659,509

© CURRENT APPLICATION NUMBER: US/10/659,509

© CURRENT FILING DATE: 2003-09-10

§ NUMBER OF SEQ ID NOS: 14

§ SEQ ID NO 2

LENGTH: 4
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Sequence 801, Application US/10245871
| Publication No. US20030235594A1
| GENERAL INFORMATION:
| APPLICANT: HUMPHRENS, ROBERT
| APPLICANT: HUMPHRENS', ROBERT
| APPLICANT: HUMPHRENS', ROBERT
| APPLICANT: WINZHEN
| TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| FILE REFERENCE: REH-2013
| CURRENT APPLICATION NUMBER: US/10/245,871
| PRIOR APPLICATION NUMBER: 10/197,000
| PRIOR APPLICATION NUMBER: 10/197,000
| PRIOR APPLICATION NUMBER: 09/396,813
| PRIOR APPLICATION NUMBER: 09/396,813
| RUMPER OF SEQ ID NOS: 905
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NOS: 905
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Ii-key/Ebola virus VP24 MHC Class II epitope
OTHER INFORMATION: hybrid peptide
FEATURE:
OTHER INFORMATION: C-term amidated
US-10-245-871-801
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Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 2; Conservative 0; Mismatches 0;
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; ORGANISM: Diploptera punctata
US-10-659-509-2
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Search completed: February 28, 2006, 09:02:03 Job time : 1.58312 secs

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Sequence 801, App
Sequence 1660, Ap
Sequence 2685, Ap
Sequence 20, Appli
Sequence 9, Appli
Sequence 9, Appli
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Sequence 3, Appli
Sequence 8, Appli
                                                                                                                                                 (without alignments)
556.876 Million cell updates/sec
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                                                                                                                         February 28, 2006, 08:56:26; Search time 0.053467 Seconds
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1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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Match Length
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No.
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7	100.0		7	JS-11-244-209-20	Sequence	
10	100.0	7 7	_	US-11-247-423-459	Sequence	ດັ
-	100.0	8	2	US-10-980-346B-43	Sequence	43, Appl
-	100.0	œ	7	US-11-045-024-1087	Sequence	1087,
30 10	100.0	60	7	US-11-045-024-1088	Sequence	1088,
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10	100.0	80	7	US-11-045-024-1090	Sequence	1090,
10	_	80	7	US-11-045-024-1091	Sequence	1091,
10	-	α)	7	US-11-045-024-1679	Sequence	1679,
5 10	٦	60	7	JS-11-045-024-2508	Sequence	2508,
10	7	60	7	US-11-045-024-2509	Sequence	2509,
Н	-	60	7	US-11-045-024-2510	Sequence	_
38 10	100.0	60	7	US-11-045-024-3503	Sequence	3503, Ap
		00	7	US-11-045-024-3504	Sequence	3504,
10	-	œ	7	US-11-045-024-3505	Sequence	
41 10		ω,	7	US-11-045-024-3506	Sequence	3506,
10	_	œ	7	US-11-045-024-4032	Sequence	4032,
10	100.0	ω	7	US-11-045-024-4033	Sequence	4033,
44 10	100.0	80	7	JS-11-045-024-4034	Sequence	4034,
10	100.0	80	7	US-11-045-024-4369	Sequence	4369,

ALIGNMENTS

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APPLICANT: PETRIS, JOSEPH S.M.
APPLICANT: PETRIS, JOSEPH S.M.
APPLICANT: PETRIS, JOSEPH S.M.
APPLICANT: POON, LIT MAN
APPLICANT: GUAN, XI
APPLICANT: GUAN, XI
APPLICANT: GUAN, XI
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REFERENCE: V0690.0031
CURRENT FILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 2918
SOFTWARE: PACENTIN version 3.2
SEQ ID NOS: 2918
SOFTWARE: PACENTIN VERSION 3.2
SEQ ID NO 1660
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TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2010/1801
CURRENT APPLICATION NUMBER: US/11/033,039
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR PILING DATE: 2002-017
PRIOR PILING DATE: 2002-017
PRIOR PLING DATE: 10/197,000
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              Sequence 1660, Application US/10895064 Publication No. US20060018923A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/11033039; Publication No. US20060002947A1; GENERAL INFORMATION: APPLICANT: HUMPHREYS, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Corononavirus-HKU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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JS-10-895-064-1660
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US-10-895-064-2685
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APPLICANT:
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| Sequence 8 Application US/11033039
| Publication No. US20060002947A1
| GENERAL INFORMATION:
| APPLICANT: HUMPHREYS, ROBERT
| APPLICANT: HUMPHREYS, ROBERT
| APPLICANT: HUMPHREYS, ROBERT
| TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| CURRENT FILING DATE: 2005-01-11
| PRIOR PELICATION NUMBER: 10/197,000
| PRIOR PELICATION NUMBER: 09/396,813
| PRIOR FILING DATE: 1999-09-14
| NUMBER OF SEQ ID NOS: 1452
| SOFTWARE: PATENTIN VERSION 3.3
| SER IN ON 8
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APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: 10/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
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                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Modified; OTHER INFORMATION: mammalian li-key peptide US-11-033-039-3
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                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 10; DB 7; I
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: Patentin version 3.3
SEQ ID NO 3
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RM 2
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APPLICANT: NICHOLLS, JOHN M.
APPLICANT: LEUNG, FREDERICK C.
TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | CENERAL INFORMATION: APPLICANT: YUEN, KWOK YUNG |
| APPLICANT: YUEN, KWOK YUNG |
| APPLICANT: YUEN, KWOK YUNG |
| APPLICANT: HAU, KAR PUI SUSANNA |
| APPLICANT: HAU, KAR PUI SUSANNA |
| APPLICANT: CHAN, KWOK HUNG |
| APPLICANT: CHAN, KWOK HUNG |
| APPLICANT: POON, LIT NAN |
| APPLICANT: POON, LIT NAN |
| APPLICANT: PEIRIS, JOSEPH S.M. |
| APPLICANT: PEIRIS, JOSEPH S.M. |
| APPLICANT: PEIRIS, THEREOF |
| TITLE OF INVENTION: INPECTION AND USES THEREOF |
| TITLE OF INVENTION: INPECTION AND USES THEREOF |
| TITLE OF INVENTION: INPECTION AND USES THEREOF |
| TITLE OF INVENTION: INPECTION AND USES THEREOF |
| TITLE OF INVENTION: INPECTION AND USES THEREOF |
| TITLE OF INVENTION: INPECTION AND USES THEREOF |
| TITLE OF INVENTION: INPECTION AND USES THEREOF |
| TITLE OF INVENTION INVERSE: 10/895,064 |
| RICOR FILING DATE: 2004-07-21 |
| NUMBER OF SEQ ID NOS: 4257 |
| SOFTWARE: PATENTIN VERSION 3.3 |
| SEQ ID NO 1660 |
                                                                                                                                                                                                                                                                                                       ; FEATURE:
; CTHER INFORMATION: Description of Artificial Sequence: Synthetic
; CTHER INFORMATION: hybrid peptide
US-11-033-039-801
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Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indel
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PATENTIN Version 3.3
SEQ ID NO 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2685, Application US/10895064; Publication No. US20060018923A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1660, Application US/11129741; Publication No. US20060034853A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PETRIS, JOSEPH S.M. APPLICANT: YUEN, KWOK YUNG APPLICANT: POON, LIT MAN
                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Corononavirus-HKU1
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Best Local Similarity 100.0
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APPLICANT: Wang, Xiaoju
TITLE OF INVENTION: Phage Microarray Profiling of the Humoral Response to Disease
FILE REFERENCE: UM-09899
CURRENT APPLICATION NUMBER: US/11/145,861
CURRENT FILING DATE: 2005-06-06
SUMUMBER OF SEQ ID NOS: 464
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-09-17
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 1999-09/396,813
PRIOR FILING DATE: 1999-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Modified
OTHER INFORMATION: mammalian 11-key peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 10; DB 7; Length 5; 100.0%; Pred. No. 8.2e+04;
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NUMBER OF SEQ ID NOS: 16
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 9
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Publication No. US20060014138A1
GENERAL INFORMATION:
APPLICANT: Chinnaiyan, Arul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHERYS, ROBERT
APPLICANT: XU, MINZHEN
                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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SOFTWARE: Patentin version 3.3
SEQ ID NO 9
LENGTH: S
                                                                                                                                                                       OTHER INFORMATION: Synthetic US-11-191-574-9
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Best Local Similarity 100.
Matches 2; Conservative
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Matches 2; Conservative
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LOCATION: (5)..(5)
OTHER INFORMATION: Ava
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US-11-145-861-365
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
TITLE OF INVENTION: AUTOIMMUNE DISEASES
FILE REFERENCE: 21417-98470
CURRENT APPLICATION NUMBER: US/11/062,186
CURRENT APPLICATION NUMBER: G0/546,062
PRIOR PILING DATE: 2004-02-18
PRIOR PILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 172
SEQ ID NO 20
LENGTH: 5
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APPLICANT: Hoeg-Jenen, Thomas
APPLICANT: Balschmidt, Per
APPLICANT: Balschmidt, Per
APPLICANT: Markuseen, Jan
APPLICANT: Diers, Ivan
TITLE OF INVENTION: Method for Making Acylated Polypeptides
FILE REPERENCE: 6305.200-40
FILE REPERENCE: 6305.200-40
FRIOR APPLICATION NUMBER: US/11/191,574
CURRENT APPLICATION NUMBER: US/10/205,270
FRIOR FILING DATE: 2002-07-24
FRIOR FILING DATE: 2001-07-24
FRIOR FILING DATE: 2001-07-24
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Pred. No.
                                           CURRENT APPLICATION NUMBER: US/10/895,064
CURRENT FILING DATE: 2004-07-21
NUMBER OF SEQ ID NOS: 2918
SOFTWARE: Patentin version 3.2
SEQ ID NO 2685
LENGTH: 5
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Publication No. US20050272097A1
GENERAL INFORMATION:
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Publication No. US20050272125A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                100.0%;
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US-10-895-064-2685
  TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity 100.
Matches 2; Conservative
                       FILE REFERENCE: V0690.0031
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ORGANISM: Homo sapiens
US-11-062-186-20
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PRIOR APPLICATION NUMBER: 60/393,211
PRIOR APPLICATION NUMBER: 60/393,211
PRIOR PILING DATE: 2002-07-01
PRIOR FILING DATE: 2002-07-01
PRIOR FILING DATE: 2002-07-01
PRIOR PLICATION NUMBER: 60/393,233
PRIOR PILING DATE: 2002-07-01
PRIOR PLILING DATE: 2002-07-01
PRIOR PLING DATE: 2002-07-01
PRIOR PLING DATE: 2002-07-01
PRIOR PLING DATE: 2002-07-01
PRIOR PLING DATE: 2002-12-04
PRIOR PLING DATE: 2002-12-04
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FILING DATE: 2002-07-01
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ORGANISM: Homo sapiens
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US-11-249-847-51
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Sequence 51, Application No. US20060035270A1

GENERAL INFORMATION:
APPLICANT: Hee, Frank D.
APPLICANT: Chan, John W.
APPLICANT: Chan, John W.
APPLICANT: Benkovic, Stephen J.
TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVENTION UNMBER: US/11/249,847

CURRENT APPLICATION NUMBER: US/11/249,847

CURRENT FILING DATE: 2005-10-12

PRIOR APPLICATION NUMBER: 60/379,626

PRIOR PILING DATE: 2002-05-10

PRIOR PILING DATE: 2002-05-10

PRIOR PILING DATE: 2002-07-01

PRIOR PILING DATE: 2002-07-01

PRIOR PILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: 60/393,137
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j Sequence 2665, Application US/11129741

j Publication No. US20060034853A1

j GENERAL INFORMATION:
APPLICANT: VUEN, KWOK YUNG
APPLICANT: HOW, CHIU YAT PATRICK
APPLICANT: HOW, CHIU YAT PATRICK
APPLICANT: HOW, CHIU YAT PATRICK
APPLICANT: GOON, LIT MAN
APPLICANT: GOON, LIT MAN
TITLE OF INVENTION: INPECTION AND USES THEREOF
TITLE OF INVENTION: INPECTION AND USES THEREOF
FILE REFERENCE: V0690.0044
CURRENT APPLICATION NUMBER: US/11/129,741
CURRENT APPLICATION NUMBER: 10/895,064
PRIOR PRILING DATE: 2004-07-21

NUMBER OF SEQ ID NOS: 4257

SEQ ID NO 2685
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100.0%; Score 10; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels
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Corononavirus-HKU1
US-11-129-741-2685
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Best Local Similarity 100.
Matches 2; Conservative
             ; SEQ ID NO 365
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-145-861-365
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US-11-249-847-493
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APPLICANT: Lee, Frank D.
APPLICANT: Lee, Frank D.
APPLICANT: Chang, Shengsheng
APPLICANT: Chang, Shengsheng J.
APPLICANT: Chang, Shengsheng J.
APPLICANT: Chang, Shengsheng J.
TITLE OF INVERTION: UNIQUE RECCANITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVERTION: UNIQUE RECCANITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVERTION: UNIQUE RECCANITION SEQUENCES AND METHODS OF USE THEREOF IN TITLE OF INVERTION: 10/43,549
FILE REFERENCE: EPTW-P06-001
CURRENT FILING DATE: 2003-06-12
FRICK PILING DATE: 2003-06-10
FRICK PILING DATE: 2003-07-01
FRICK PILING DATE: 2002-07-01
FRICK PILING DATE: 2002-07-01
FRICK APPLICATION NUMBER: 60/393,137
FRICK PILING DATE: 2002-07-01
FRICK APPLICATION NUMBER: 60/393,233
FRICK PILING DATE: 2002-07-01
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                       100.0%; Score 10; DB 7; Length 5; tilarity 100.0%; Pred. No. 8.2e+04; Conservative 0; Mismarran
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0; Mismatches 0;
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Publication No. US20060035270A1
GENERAL INFORMATION:
APPLICANT: Lee, Frank D.
APPLICANT: Meng, Dr. Xun
APPLICANT: Chan, John W.
APPLICANT: Zhang, Shengsheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 491, Application US/11249847
Publication No. US20060035270A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 2; Conservative
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CORGANISM: Homo sapiens
US-11-249-847-491
                                                                     Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-11-249-847-493
US-11-249-847-486
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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Blocceleration Ltd.

OM protein - protein search, using sw model

February 28, 2006, 08:45:35 ; Search time 0.121972 Seconds
(without alignments)
1577.691 Million cell updates/sec Run on:

US-10-717-665A-44_COPY_448_449 Title: Perfect score:

1 RM 2 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters: : 283416 ... Minimum DB seq length: 0

2)

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		T-cell receptor be	cytochilican av 1	cytochrome P450c27	hypothetical prote			pimeloyl-CoA synth	protein 0A100028 -	thyrotropin-releas	protein-tyrosine k	heat shock protein	photosystem II 6.1	c	homeotic protein G	ribosomal protein	77		glutathione transf		glutathione transf	e t	crystallin - Pacif	allerge n	GroEL protein homo		light-harvesting p	serum heterodimer,
8	PT0298	PT0670	PC4442	A42324	T44420	PC1215	H83778	A56786	PA0020	A45096	S24667	S11805	A41170	S78415										A4477	PC438	PC438	E5422	A56899
Length DB	9 2			121				15 2												0	0	0	0	0	20 2	0	0	20 2
ery tch	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	10	10	10	9 9	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
		0	m •	4 10	· v	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

T.c.i. receptor beta chain V-D-J region (121-1BN) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Nus musculus (house mouse)
C;Date: 17-301-1992 #sequence_revision 17-301-1992 #text_change 30-May-1997
C;Accession: PT0670
R;Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0670

PT0670

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Query Match
100.0%; Score 10; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels

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A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-9 <FEE>
A;Cross-references: UNIPARC:UPI000017C7EC
C;Keywords: T-cell receptor

			0000000000000	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0100000000000000	A55899 JC00099 B584355 H484135 H48413 A12535 A12535 H33262 H33262 H33262 H33262 H34801	999 1735 1735 1735 1735 1736 173 173 173 174 176 176 176 177 177 178 179 179 179 179 179 179 179 179 179 179	basement membrane phospholipase A2 (relaxin chain A - glutentione transf cryptdin - mouse (cryptdin - western probable acr 2 reg kinase-related tra heterodisulfide re glutenhione transf protein phosphatas heparin-binding gr heparin-binding gr hypothetical prote ribosomal protein ribosomal protein
PESULT 1 PRESULT 1 PRO298 Ig heavy chain CRD3 region (clone 5-103A) C; Species: Homo sapiens (man) C; Date: 30-Sep-1993 #sequence_revision 30-C; Accession: PT0298 R; Yamada; M; Wasserman, R; Reichard, B.A J. Exp. Med. 173, 395-407, 1991 A; Title: Preferential utilization of special A; Reference number: PT0222; MUID:91108337; A; Accession: PT0228 A; Molet type: DNA A; Residues: 1-8 < YAM>A; Residues: 1-8 < YAM>A; Experimental source: B lymphocyte C; Keywords: heterotetramer; immunoglobulin Query Match Best Local Similarity 100.0%; Score 1 Best Local Similarity 100.0%; Pred: N Matches 2; Conservative 0; Misma	chain (1.2 km) (1.3 k	n CRD3 reg mo sapiens pp.1993 #sec Pr.1993 #sec Wasserman Wasserman 173, 395-4 erential un umber: PTO: PTO: PTO: PTO: PTO: PTO: PTO: PTO:	D3 region (c apiens (man) 93 #sequence 98 serman, R.; 139-407, 19 139-407, 19 139-407, 19 139-407, 19 140-111; 199-8 198	man) man) ence R.; 11;za 11;za 2; M 11;mp 13; 1 100 tive	(clone an) nce_rev nce	e 5-103A) vision 30 chard, B n of spec :91108337 00017C208 yte noglobuli ; Score ; Pred. 0; Mism	RESULT 1 PP1028 Igh heavy chain CRD3 region (clone 5-103A) - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change C;Accession: PT029 R;Yamada; M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A C; Exp. Med. 173, 395-407, 1991 A;Title: Preferential utilization of specific immunoglobulin hea A;Reference number: PT0222; MUID:91108337; PMID:1899102 A;Accession: PT0222; MUID:91108337; PMID:1899102 A;Accession: PT0223 A;Accession: PT0222; MUID:91108037; PMID:1899102 A;Accession: PT0222; MUID:91108037; PMID:1899102 A;Experimental source: B lymphocyte C;Keywords: heterotetramer; Immunoglobulin Query Match Best Local Similarity 100.0%; Score 10; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 2.88+05; Matches 2; Conservative 0; Mismatches 0; Indels	RESULT 1 Pr0298 Pr0298 Pr0298 Pr0298 C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: For Sapiens (ma
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hypothetical protein BH1032 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date. 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Date. 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H83778
B;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and can sheef the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the se
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C;Species: Echinococcus granulosus
C;Species: Bchinococcus granulosus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: PC1215
R;Oliver, G; Vispo, M; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlich
Gene 121, 337-342, 1992
A;Title: Homeoboxes in flatworms.
A;Reference number: JC1386; MUID:93077050; PMID:1359988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CjAccession: T44420
R;Vlaskova, H.; Krasny, L.; Fucik, V.; Jonak, J.
Submitted to the EMBL Data Library, September 1997
Submitted to the EMBL Data Library, September 1997
Submitted to the EMBL Data Library, September 1997
Submitted to the EMBL Data Library, September 1997
A;Reference number: 222760
A;Reference number: 222760
A;Reference number: Z22760
A;Reference number: Z22760
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A;Experimental source: strain CCM 2184
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein [imported] - Bacillus stearothermophilus (fragment) C;Species: Bacillus stearothermophilus C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 18+03;
Matches 2; Conservative 0; Mismatches 0; Indels
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                                                    Indels
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A;Molecule type: DNA
A;Residues: 1-14 < OLL5
A;Cross-references: UNIPARC:UPI000017B68F; EMBL:X66821
C;Keywords: homeobox
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100.0%; Pred. No. 9.1e+02; ive 0; Mismatches 0;
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          Best Local Similarity 100.
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A;Status: preliminary
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Feb-1996
C;Accession: A42324
R;Shayiq, R.M.; Avadhani, N.G.
J. Biol. Chem. 267, 2421-2428, 1992
A;Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat mitod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Rolecule type: 1-11 <BRY>
A;Cross-references: UNIPARC:UPI000017ABC5
C;Comment: This protein, one of the eleven components detected in this species of the ph
C;Keywords: photosystem II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vincourse Journal of Communiar, R.; Guglielmi, G.; Stevens Jr., S.E.
Arch. Microbiol. 153, 550-560, 1990
A; Title: Structural and compositional analyses of the phycobilisomes of Synechococcus sp
                                                                                                                                                                                                                                cyrocarrome 233 - Desultovibrio desulfuticans
cypecies: Desulfovibrio desulfuticans
c;Species: Desulfovibrio desulfuticans
c;Date: 28-Mar-1998 #sequence_revision 28-Mar-1998 #text_change 09-Jul-2004
C;Accession: PC4442
R;Aubert, C.; Leroy, G.; Bianco, P.; Forest, E.; Bruschi, M.; Dolla, A.
Biochem. Blophys. Res. Commun. 242, 213-218, 1998
A;Title: Characterization of the cytochromes C from Desulfovibrio desulfuricans G201.
A;Reference number: PC4442
A;Molecule type: protein
A;Residues: 1-10 < AUB>
A;Cross-references: UNIPROT:Q7MOW6; UNIPARC:UP1000017AB62
A;Experimental source: strain G201
C;Comment: This protein is involved in the formate reduction pathway.
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C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C;Accession: E60691
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <SHA>
A;Cross-references: UNIPARC:UPI000017C8FA
A;Note: sequence extracted from NCBI backbone (NCBIN:78404, NCBIP:78410)
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Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 2; Conservative 0; Mismatches 0; Indels
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A;Accession: E60691
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                                                                                                                                                                                      cytochrome c553 - Desulfovibrio desulfuricans (fragment)
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100.0%; Score 10; DB 2; L
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 2; Conservative 0; Mismatches 0;
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0; Indels

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Best Local Similarity 100. Matches 2; Conservative

Query Match

1 RM 2

ઠે 셤 pimeloyl-CoA synthase - Bacillus sphaericus (fragment)

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thyrotropin-releasing hormone receptor, splice form 387 - rat (fragment)
C,Species: Rattus norvegicus (Norway rat)
C,Species: Rattus norvegicus (Norway rat)
C,Species: Rattus norvegicus (Norway rat)
C,Species: A55096
R;de la Pena, P.; Delgado, L.M.; del Camino, D.; Barros, F.
J. Balo. Chem. 267, 25703-23708, 1992
A,Title: Two isoforms of the thyrotropin-releasing hormone receptor generated by alternat A;Reference number: A45096
A,Faccession: A45096
A,Sccession: A5096
A,Status: preliminary; not compared with conceptual translation
A,Wolecule type: mRNA
A,Residues: 1-15 - DEL>
A,Facessione: CFP: NIDPARC:UPI0000170C44; GB:S51512; NID:g261982; PIDN:AAB24549.1; PID:gA;Reperimental source: GH3 anterior pituitary cells
A,Rote: sequence extracted from NCBI backbone (NCBIP:120927)
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C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 13-Mar-1997 #text_change 04-Feb-2000
C;Accession: S24667
R;Sorrentino, V.
Submitted to the EMBL Data Library, May 1992
A;Reference number: S24666
A;Accession: S24667
A;Accession: S24667
A;Accession: S24667
A;Return: preliminary
A;Molecule type: DNA
A;Resious: 1-16 <SONA
A;Resious: 1-16 <SONA
A;Resious: 1-16 <SONA
A;Resious: ATP; phosphotransferase; tyrosine-specific protein kinase
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C;Species: Comamonas acidovorans
C;Species: Comamonas acidovorans
C;Accession: S11805; 822676
R;Hallett, P.; Mehlert, A.; Maxwell, A.
Mol. Microbiol. 4, 345-353, 1990
A;Title: Escherichia coli cells resistant to the DNA gyrase inhibitor, ciprofloxacin, ove A;Reference number: S11805; MuID:90286912; PMID:1972534
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A; Residues: 1-16 (4ML).
A; Residues: 1-16 (4ML).
A; Cross-references: UNIPROT: Q9R5K5; UNIPARC: UPI000017A951
A; Note: the species identification has been revised in reference S22676
R; Fowell, S.L.; Lilley, K.S.; Jones, D.; Maxwell, A.
Mol. Microbiol: 6, 1575-1576, 1992 Pseudomonas species.
A; Title: GroEL proteins from three Pseudomonas species.
A; Reference number: S22676; MUID: 921326643; PMID: 1352616
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100.0%; Score 10; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
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100.0%; Score 10; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
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                                                                         A,Residues: 1-14 <STO>
A,Cross-references: UNIPROT:Q9KE26; UNIPARC:UPI0000C3A89; GB:AP001510; GB:BA000004; NID
A,Cross-references: UNIPROT:Q9KE26; UNIPARC:UPI0000C3A89; GB:AP001510; GB:BA000004; NID
A,SExperimental source: strain C-125
C,Genetics:
A,Gene: BH1032
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C.Jate: 3D-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C.Jacession: PA0020
R.Jacession: PA0020
R.Jacession: PA0020
R.Jacession: PA0020
A.Jacession: A. Rawakami, T.; Miyatake, N.; Tsugita, A.
B.Jacession: N.; Kawakami, T.; Miyatake, N.; Tsugita, A.
A.Jacession: Separation and characterization of Arabidopsis proteins by two-dimensiona
A.Reference number: PA0001
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R;Ploux, O.; Soularue, P.; Marquet, A.; Gloeckler, R.; Lemoine, Y.
Biochem. J. 287, 685-690, 1992
A;Title: Investigation of the first step of biotin biosynthesis in Bacillus sphaericus.
A;Reference number: A56786; MUID:93075017; PMID:1445232
A;Accession: A56786
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A;Note: sequence extracted from NCBI backbone (NCBIP:117639)
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C.Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Aug-1995
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A, Gene: blow C, Keywords: blotin blosynthesis; homodimer

C;Genetics

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A; Cross-references: UNIPARC: UPI000017ACA8

protein QA100028 - Arabidopsis thaliana (fragment)

A;Molecule type: protein
A;Mesidues: 1-15 «KAM»
A;Cross-references: UNIPARC:UPI000017AFE7
A;Experimental source: callus

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8 유 RESULT 11 A45096

Accession: PA0020

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RESULT 14

photosystem II 6.1K protein - Chlamydomonas reinhardtii (fragment)

photosystem II 6.1K protein - Chlamydomonas reinhardtii (c;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
R;de Vitry, C.; Diner, B.A.; Popot, J.L.
J. Biol. Chem. 266, 16614-16621, 1991
J. Biol. Chem. 266, 16614-16621, 1991
A;Fitle: Photosystem II particles from Chlamydomonas reinhardtii. Purification, molecula A;Reference number: A41170; MUID:91358452; PMID:1885590
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Matches 2; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
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100.0%; Score 10; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
A;Note: the source is designated as Pseudomonas acidovorans C;Genetics:
A;Gene: groEL
C;Keywords: molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 < CEV.
A;Cross-references: UNIPROT:Q7MlJ4; UNIPARC:UPI000017AF05
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Search completed: February 28, 2006, 08:54:19 Job time : 1.12197 secs

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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae; Laurus.
NCBI_TaxID=85223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=15598737; DOI=10.1073/pnas.0408336102;
Bergthorsson U., Richardson A.O., Young G.J., Goertzen L.R.,
Palmer J.D.;
"Massive horizontal transfer of mitochondrial genes from diverse land
plant donors to the basal angiosperm Amborella.";
Proc. Natl. Acad. Sci. U.S.A. 101:17747-17752(2004).
EMBL, AY832169; AN31502.1; -; Genomic_DNA.
GO; GO:0005739; C:mitochondrion; IEA.
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Q5IA47.
10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
NADH dehydrogenase subunit 4 (Fragment).
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Last sequence update)
Last annotation update)
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04 VN45 FUGRU
09 AXV9 BRADL
09 AXW2 BRADL
09 AXW2 BRADN
09 AXW2 BRADN
07 MUC9 BAT
09 00 W74 9 WUR I
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07 6 MUCA
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QSUU76 PLACH
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Homo sapiens (Human).
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    000000000000000
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AC QOUKGG;
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  NCBI_TaxID=9606;
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"Massive horizontal transfer of mitochondrial genes from diverse land plant donors to the basal angiosperm Amborella."; proc. Natl. Acad. Sci. U.S.A. 101:17747-17752(2004). EMBL; AY832171; AAW31504.1; -; Genomic_DNA.
                                                                         "Massive "D.C.",
"Massive borizontal transfer of mitochondrial genes from diverse land plant donors to the basal angiosperm Amborella.";
Proc. Natl. Acad. Sci. U.S.A. 101.17747-1752(2004).
EMBL; AY832172; AAM31505.1; -; Genomic_DNA.
GO, GO:0005739; C:mitochondrion; IEA.
Mitochondrion.

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9 AA; 996 MW; D35B7772C8768412 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
PubMed=15598737; DOI=10.1073/pnas.0408336102;
Bergthorsson U., Richardson A.O., Young G.J., Goertzen L.R.,
NUCLEOTIDE SEQUENCE.
PubMed=15598737; DOI=10.1073/pnas.0408336102;
Bergthorsson U., Richardson A.O., Young G.J., Goertzen L.R.,
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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10-MAY-2005 (TrEMBLrel. 30, Last annota
10-MAY-2005 (TrEMBLrel. 30, Last annota
NADH dehydrogenase subunit 4 (Fragment)
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Mitochondrion.
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Q7MOM6;
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QSIA45;
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Berthman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
James K., Rutherford K., Harris B., Harris D., Churcher C.,
Quali M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
"A comprehensive survey of the Plasmodium life cycle by genomic,
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Araceae, Aroideae, Philodendreae, Philodendreae, Philodendron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcriptomic, and proteomic analyses.";
Science 307:82-86(2005).
-1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
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Similarity 100.0%; Score 10; DB 2; Length 9;
Similarity 100.0%; Pred. No. 2.2e+06;
2; Conservative 0; Mismatches 0; Indels
        Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIS9087; AAF04001.1; -; Genomic_DNA.
GO; GO:0004872; F:receptor activity; IEA.
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
                                                                                                NON TER 1 1
NON TER 9 9
SEQUENCE 9 AA; 1272 MW; 6F2B8415B331E684 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Hypothetical protein (Fragment).
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EMBL; CAAJ01000035; CAH74304.1; -; Genomic_DNA
Hypothetical protein.
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OSIA44 9ARAE

ID Q5IA44 9ARAE PRELIMINARY;

DT 10-MAY-2005 (TrEMBLrel. 30,

DT 10-MAY-2005 (TrEMBLrel. 30,

DT 10-MAY-2005 (TrEMBLrel. 30,

DT 10-MAY-2005 (TrEMBLrel. 30,

DE NADH dehydrogenase subunit 4

GN Name=nad4;

OS Philodendron oxycardium.

OG Mitochondrion.

OG Mitochondrion.

OG Spermatophyta; Magnoliophyte

OC Philodendreae; Philodendron.

OX NOBI TAXID=71614;
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Q4y954 PLACH PRELIMINARY;
Q4Y954;
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Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.

Cytochrome c553 (Fragment). Desulfovibrio desulfuricans

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revealed in the avian genome.";
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QBJJ33;
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Q709B0_HUMAN PRELIMINARY;
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Myelin proteolipid protein (Fragment).
Ficedula albicoliis (Collared flycatcher).
Ficedula albicoliis (Collared flycatcher).
Archosauria; Aves; Neognathae; Craniata; Wusticapidae; Ficedula.
NCDI TaxID=59894;
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Chauviere M., Martinage A., Debarle M., Sautiere P., Chevaillier P.;
"Molecular characterization of six intermediate proteins in the
processing of mouse protaine P2 precursor.";
Eur. J. Biochem. 204:759-765(1992).
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Primmer C.R., Barge T., Lindell J., Saetre G.P.;
"Single-nucleotide polymorphism characterization in species with
limited available sequence information: high nucleotide diversity
                            MEDLINE-998102111; PubMed=9439638; DOI=10.1006/bbrc.1997.7852; Aubert C., Lercy G., Bianco P., Forest E., Bruschi M., Dolla A.; "Characterization of the cytochromes C from Desulfovibrio desulfuricans G201.";
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PIR; PC4442; PC4442.
NON TER 10 10 10 SEQÜENCE 10 AA; 1112 MW; 87C51E5735BDD87A CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Q9QVP1_9MURI PRELIMINARY;
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QGJFE7 FICAL PRELIMINARY;
QBJFE7;
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 NCBI_TaxID=876;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
NCBI_TaxID=46689;
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MUCLEOTIDE SEQUENCE.

PRIBLINE-21918460. PubMed=11918793;

Primmer C.R., Borge T., Lindell J., Saetre G.P.;

"Single-nucleotide polymorphism characterization in species with
"Single-nucleotide sequence information: high nucleotide diversity revealed in the avian genome.";

Mol. Ecol. 11:603-612(2002).
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10 AA; 1206 MW; 1FAAC9676732C86B CRC64;
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01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-0cT-2002 (TrEMBLrel. 22, Last annotation update)
Myelin proteolipid protein (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
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100.0%; Pred. No. 3.8e+03;
ative 0; Mismatches 0;
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MO1. ECO1. 11:603-612(2002).
EMBL; AF454217; AAM22903.1; -; Genomic DNA.
EMBL; AF454218; AAM22904.1; -; Genomic DNA.
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NON TER 1 1
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SEQÜENCE 12 AA; 1442 MW; 7500ECB95A172684 CRC64;
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Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0;
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P95606 ALCEU PRELIMINARY;
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Theor. Appl. ARK0666.1; -; Genomic_DNA.

GO: GO: 00008020; F:G-protein coupled photoreceptor activity; IEA.

GO; GO: 00009585; P:red, far-red light phototransduction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=12582899;
Fourmann M., Barret P., Froger N., Baron C., Charlot F., Delourme R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                              Gaps
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Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                  100.0%; Score 10; DB 2; Length 11; 100.0%; Pred. No. 4.2e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2005) to the EMBL/GenGanic_DNA. 12 12 12 12
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01-UNN-2001 (TrEMBLrel. 17, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
Phytocome A (Fragment).
                                                                                                             11 AA; 1276 MW; 7BB98CBD07287044 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Transcription factor EB (Fragment).
Name=TFEB; ORFNames=RP4-696P19.3-012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 AA
      Nucleic Acids Res. 32:2315-2322 (2004).
EMBL; AJ608782; CAE77674.1; -; mRNA.
EMBL; AJ608782; CAE77677.1; -; mRNA.
EMBL; AJ608788; CAE77673.1; -; mRNA.
NON TER
11 11
SEQÜENCE 11 AA; 1276 MW; 7BB98GED0
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                                                                                                                                                                                                                                                                                                                                                                                    Q4VXX2_HUMAN PRELIMINARY;
Q4VXX2;
                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 2; Conservative
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Q4VXX2_HU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                         Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Cupriavidus.
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
NCBI_TaxID=1422;
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12 AA; 1367 MW; 478C45052BC87DD7 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                      01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Nickel permease (Fragment).
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12
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PRT;
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Q9TQS4 HORSE

ID Q9TQS4 HORSE PRELIMINARY; PRT; 13 AA.

AC Q9TQS4

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)

DT 1-FEB-2005 (TrEMBLrel. 29, Last annotation update)

E Transferrin (Fragment).

DE Transferrin (Fragment).

C Equus caballus (Horse).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

C Mammalia; Lutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.

C NCBI_TAXID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                          Query Match 100.0%; Score 10; DB 2; Length 12; Best Local Similarity 100.0%; Pred. No. 4.6e+03; Matches 2; Conservative 0; Mismatches 0; Indels
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Giffard J.M., Brandon R.B., Bell T.K.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; ARI88755; AAR05469.1; -; Genomic_DNA.

EMBL; AR185754; AAF05468.1; -; Genomic_DNA.

NON_TER 1 1 1

NON_TER 13 13

SEQUENCE 13 AA; 1528 MW; D379D35F2EA2840D CRC64;
EMBL; AJ01805; CAA05021.1; -; Genomic_DNA.
PIR; T44420; T44420.
Hypothetical protein.
NON TER 12 12
SEQUENCE 12 AA; 1379 MW; 70087CB0E8A6840B CRC64;
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Search completed: February 28, 2006, 08:53:04 Job time: 2.7335 secs

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Bioccele:	5.1.7 Biocceleration Ltd.
OM protein - protein search, using sw model	
Run on: February 28, 2006, 08:37:25 ; Search (without a 1282.772 M	. Search time 36.9925 Seconds (without alignments) 1282.772 Million cell updates/sec
Title: US-10-717-665A-44_COPY_532_639 Perfect score: 551 Sequence: 1 KLAFRACKLKKKAQYEANKVTAEGNPTGGLVGLRIPTSKV 108	TGGLVGLRIPTSKV 108
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched: 2443163 segs, 439378781 residues	
Total number of hits satisfying chosen parameters:	2443163
Minimum DB seq length: 0 Maximum DB seq length: 200000000	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
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Pred. No, is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adk65805 Angiogene	Ado20373 Human PRO	Abb68374 Drosophil	Abg29275 Novel hum	Abull886 Human ABC	Abu19277 Protein e	Abu01541 S. pneumo	Adm92163 S pneumon	Ads44237 Bacterial		Abu43663 Protein e	Ads30054 Bacterial		Adn04305 Antipsori	Abu61812 Human nuc		1 Human	Ads88212 Human pro	Abm85413 Human pro	Human	Aab40574 Human ORF	Aab48935 Brassica	Adk47294 Streptoco	Adr94210 Novel S.
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SUMMARIES	ID	ADK65805	AD020373	ABB68374	ABG29275	ABU11886	ABU19277	ABU01541	ADM92163	ADS44237	ADS3 0935	ABU43663	ADS30054	AAW18226	ADN04305	ABU61812	ADG86291	ADQ18921	ADS88212	ABM85413	ADG86299	AAB40574	AAB48935	ADK47294	ADR94210
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	Score	551	543	202	200.5	82	78.5	75.5	75.5	75.5	74.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	72.5		
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The invention relates to a method of determining the angiogenic index of a tissue or cell sample comprising assessing, in a sample, the expression levels of one or more differentially-expressed gene from any of 34 DNA sequences, given in the specification, where the levels are indicative of the angiogenic index. The methods and compositions of the present

Claim 23; SEQ ID NO 44; 296pp; English.

Aea58080 Streptoco	Adn20856 Bacterial	Abb65505 Drosophil	Adn26279 Bacterial	Adn22598 Bacterial	Adn22599 Bacterial	Adk64278 Disease,t	Aag67384 Amino aci	Adn20612 Bacterial	Adv16175 X. pelarg	Aag67386 Amino aci	Adn20163 Bacterial	Ady86677 Human GRP	Ady86676 Human GRP	_	Adn99816 Novel hum	Adf77333 Heat shoc	Aae23607 Human end	Abp26389 Streptoco	Abu46647 Protein e	Adn99815 Novel hum
AEA58080	ADN20856	ABB65505	ADN26279	ADN22598	ADN22599	ADK64278	AAG67384	ADN20612	ADV16175	AAG67386	ADN20163	ADY86677	ADY86676	ADN72115	ADN99816	ADF77333	AAE23607	ABP26389	ABU46647	ADN99815
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651	861	505	825	1355	1355	667	487	597	640	846	1105	152	188	190	194	220	223	282	282	287
3.2	3.1	2.9	5.9	5.9	5.0	12.8	2.7	12.7	2.7	2.7	5.6	2.5	2.5	2.5	2.5	2.5	2.5	12.5	2.5	2.5
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72.5	72	7.1	71	71	71	70.5	70	70	70	70	69.5	69	69	69	69	69	69	69	69	69
25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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cytostatic; cardiant; vasotropic; antiarteriosclerotic; angiogenesis inhibitor; angiogenesis stimulator; angiogenesis stimulator; angiogenec; gene expression; cancer; coronary artery disease; myocardial ischemia; coronary arteriosclerosis; forensic medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the angiogenic index of a tissue or cell sample using expression levels of differentially expressed genes, useful for diagnosing or treating cancer, coronary artery disease, myocardial ischemia and/or arteriosclerosis.
                                                                              Angiogenesis-differentially expressed protein ANH0757.
                                                                                                                                                                                                                                                                                                                                                         Jay G;
          ADK65805 standard; protein; 639 AA.
                                                                                                                                                                                                                                                                                                                                                        Li X, Kovacs KF, Fan W,
                                                                                                                                                                                                                                                                                                                                  (ORIG-) ORIGENE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                    07-FEB-2002; 2002US-00067482.
10-JUN-2002; 2002US-00164595.
16-AUG-2002; 2002US-0403649P.
03-JAN-2003; 2003US-0437746P.
                                                                                                                                                                                                                                              07-FEB-2003; 2003WO-US003848.
                                                         (first entry)
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N-PSDB; ADK65804.
                                                                                                                                                                                             WO2003066831-A2.
                                                          06-MAY-2004
                                                                                                                                                                       Homo sapiens
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                                  ADK65805;
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ADK6580
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                                                                                                                                                                                                       532 KLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
invention are useful for diagnosing, preventing and/or treating cancer, coronary artery disease, myocardial ischemia or coronary arteriosclerosis. They can also be used in research, drug discovery and forensic medicine involving angiogenesis. This sequence corresponds to one of the differentially expressed proteins of the invention.
                                                                                                                                                                          1 KLAFRACRIKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ
                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                               ADO20373 standard; protein; 296 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO polypeptide #633
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                        Query Match
Best Local Similarity 100.
Matches 108; Conservative
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N-PSDB; ADO20372.
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                                                                                           Sequence 639 AA;
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                                                                                                                                      Best Local
Matches
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The invention relates to human PRO polypeptides and the polymucleotides encoding them. The polypeptides and polymucleotides are useful for treating and disgnoshing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, sjoyeren's syndrome, vasculitis, arcoidosis, sutoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the

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                                                                                                                                                                                                            189 KLASRACRLKKKRAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNWGQ 248
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central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                               1 KLAFRACKLKKKAQYBANKVKLWGLNTEXDNLLFVINSIKQEIVNRVQNPRDEKGPNMGQ
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                                                                                                                                                                                                                                               61 KLEILIKUTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                249 KLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLKIPTSKV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
Local Similarity 43.6%; Pred. No. 1e-13;
es 48; Conservative 17; Mismatches 31; Indels 1
                                                                                                                 Length 296;
                                                                                                               98.5%; Score 543; DB 8; Length 29
99.1%; Pred. No. 3.5e-53;
iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 31914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD, Myers EW;
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                                                                                                                                                                                                                                                                                                                                                                       ABB68374 standard; protein; 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                  Best Local Similarity 99.1 Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
N-PSDB; ABL12477.
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                                                                                     Sequence 296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions
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                                                          invention
                                                                                                                        Query Match
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Matches
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ABB68374
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Gaps

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Indels

Pred. No. 1.9e-14; 2; Mismatches 12;

73.0%;

Best Local Similarity 73.0 Matches 46; Conservative

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed centry of (II) is useful in gene therapy techniques to restore normal certifying of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers; and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in disponsites, forenises, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. Abg00010-Abg30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                     1 KLAFRACRLKKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                   n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                        102
                                                                                            61 KLE-----ILIKDILGLPVAGQISEFVNQVLEKTAEGNPIGGLVGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 59634; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #29266.
                                                                                                                                                                                                     ABG29275 standard; protein; 160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS93462
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                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oiodiversity
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                                                                                                                                                                                                                                                                                                                                                       Human;
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The present invention relates to high throughput screening assays for agents capable of modulating the activity of ATP-binding cassette transporter I (ABCA), also called cholesterol efflux regulating protein (CERP)). The method comprises determining the activity of an ABCA1 polypeptide in the presence of an ABCA1-interacting protein (AIP) that polypeptide in the presence of an ABCA1-interacting protein (AIP) that modulators of ABCA1 biological activity, particularly for identifying agents that modulate cholesterol or phospholipid levels in an animal. The method is useful for treating disorders of IBCA method: sepecially for reducing elevated plasma phospholipid or cholesterol levels in a patient at risk of developing disorders such as cardiovascular in a patient at risk of developing disorders such as cardiovascular disease. (CDD), coronary artery disease (CAD), cerebrovascular disease, coronary restenosis, and peripheral vascular disease. The present sequence represents a human AIP polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying ABCA1 (cholesterol efflux regulating protein) modulators for modulating cholesterol or phospholipid levels in animals, by determining ABCA1 activity in the presence of an agent-contacted ABCA1-interacting
9 LKKKAQYEANKVKLW-GLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIK 67
                     High throughput screening assay, ATP-binding cassette transporter 1, ABCA1; cholesterol efflux regulating protein; CBRP, AIP, human; ABCA1:interacting protein; plasma cholesterol; plasma phospholipid; lipid metabolism disorder; cardiovascular disease; CVD; CAD; coronary artery disease; cerebrovascular disease; coronary restenosis; peripheral vascular disease; anti-lipaemic.
                                                                                                                                                                                                                                                                                                                  Human ABCA1 interacting polypeptide KIAA0528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 59-63; 92pp; English.
                                                                                                                                                                                                         ABU11886 standard; protein; 1124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newman SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XENON GENETICS INC.
UNIV BRITISH COLUMBIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-2001; 2001US-0283424P.
                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                            68
                                                                         68 DTL 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                            ABU11886;
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14.9%; Score 82; DB 6; Length 1124;

Query Match

Length 160;

DB 4;

36.4%; Score 200.5;

Query Match

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The invention relates to an isolated nucleic acid comprising any one of the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC of comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense contisense nucleic acid, (2) a host cell containing the vector; (3) an isolated contisense nucleic acid, (4) an antibody capable of specifically binding contisense nucleic acid, (4) an antibody capable of specifically binding cc antisense nucleic acid, (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation; (8) required for proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound sectivity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling the extent compound; a activity; (11) a culture comprising strains in which the gene compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) determining the extent compound; activity; (11) a culture compound that inhibits the extent compound that inhibits the conficuence of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                     590 RICKLKKKAQAEANA----TAISNLLPFMEYEVHTQLMNKIK----LKGMNALFGLR 638
                                                          5 RACRIKKKAQYBANKVKIMGINTBYDNLL-FVINSIKQBIVNRVQNPRDBRGPN--MGQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind JW;
Xu HH;
                      Gaps
                      24;
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Forsyth RA,
                        27; Indels
                                                                                                                                                                               62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #4804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haselbeck R,
Yamamoto R,
Best Local Similarity 28.4%; Pred. No. 7.5; Matches 29; Conservative 22; Mismatches
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                                                                                                                                                                                                                                                                                                              ABU19277 standard; protein; 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borrelia burgdorferi
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                                                                                                                                                                                                                                                                                                                                                           ABU19277;
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Wall D,
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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a
              identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                      72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media cear infection.
                                                                                                                                                                                                                                                                                                                            proliferation of an organism. The antisense nucleic acids are useful for
                                                                                                                                                                                                                                                                                                    21 KIMGLNTEYDNLLFVIN-SIKQEIVNRVQNPRDER----GPNMGQKLEILIKDT---LGL
                                                                                                                                                                                                                                                                      23; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. pneumoniae type 4 strain protein from coding region #1117.
                                                                                                                                                                                                                                14.2%; Score 78.5; DB 6; Length 281; 31.6%; Pred. No. 3.2;
                                                                                                                                                                                                                                                                        14; Mismatches
                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae; type 4 strain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU01541 standard; protein; 345 AA.
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                                                                                                                                                                                                                                                                                                                                                                                   73 PVAGQTSEFVNQVLEK
                                                                                                                                                                                                                                                                            24; Conservative
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N-PSDB; ABX06829.
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                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                        Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200277021-A2.
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Matches
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nucleic acid cited above or fragance between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementarity define the termin of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound with the and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus preventing a disease or infection where one or streptococcus media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coling regions from the genemic sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | :| |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: | |:: |:: | |:: |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LKKKAQYEANKVK-----LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Streptococcus pneumoniae nucleic acid molecules, useful for diagnosing, treating and preventing active infections of Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39; Gaps
composition), a kit comprising first and second primers, which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibacterial; gene therapy; Streptococcus pneumoniae infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 75.5; DB 6; Length 345; 27.6%; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GOKLEILI------KD-TLGLPVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S pneumoniae antigenic protein sequence SeqID360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADM92163 standard; protein; 642 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-2003; 2003WO-US027401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 345 AA;
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                          This invention relates to novel isolated Streptococcus pneumoniae nucleic acid molecules and the antigenic polypeptides encoded by them. The invention may be useful for the production of compounds with an antibacterial activity or for gene therapy. The nucleic acid molecules, compositions and methods disclosed are useful for treating Streptococcus pneumoniae infection. The present sequence is that of an S pneumoniae protein of the invention.
                                                                                                                                                                                                                                                                      The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                     9 LKKKAQYEANKVK------LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM--
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                        39;
                                                                                                                                                                                        DB 8; Length 642;
                                                                                                                                                                                                                                                                                                                                     20; Indels
                                                                                                                                                                                                                                                                                                                   59 ----GQKLBILI------KD-TLGLPVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldman BS;
                                                                                                                                                                                                                      17; Mismatches
                                                                                                                                                                                        Score 75.5; 1
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 22667; 122pp; English.
Claim 27; SEQ ID NO 360; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADS44237 standard; protein; 1175 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacterial polypeptide #22667.
                                                                                                                                                                                        13.7%; 27.6%;
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                                                                                                                                                                        Query Match
Best Local Similarity 27.00.
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GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HINKLE G J.
SLATER S C.
                                                                                                                                                         Sequence 642 AA;
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(HINK/)
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(CHEN/)
(GOLD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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c comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with the improved plant properties, e.g. improved cold, heat or drought tolerance, to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the coll cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan condition, improved lignin production or improved galactomannan condition. Note: The sequence data for this patent did not scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LAFRACRIKKKKAQYEANKVKLWGINTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.7%; Score 75.5; DB 8; I
25.0%; Pred. No. 44;
tive 21; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 SSSLIEGVRG-----NEDGENDVLNOTRETN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGN 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADS30935 standard; protein; 1124 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2003; 2003US-00369493
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Matches 23; Conservative
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SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHEN A.
GOLDMAN B S.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1175 AA;
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(CHEN/)
(GOLD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant comprising the recombinant DNA construct and growing the transformed plant with the recombinant DNA construct and growing the transforming a plant with the recombinant DNA construct is useful for improving plants with the recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with construct to plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved justed by modification of carbohydrate, nitrogen or content, improved plant growth and development under at least one stress providing improved plant growth and development under at least one stress providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form the form term of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 GLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 74.5; DB 8; Length 1124;
; Pred. No. 54;
11; Mismatches 37; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein encoded by Prokaryotic essential gene #29190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              format from USPTO at segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 GOT-SEFVNOVLEKT-AEGNPTGGLVGLRIP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 GYTLDEIKNDITKKTPASFEPTIDYVVTKIP 399
                                                                                                claim 1; SEQ ID NO 19968; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU43663 standard; protein; 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001US-00815242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.5%;
28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus haemolyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2001; 2
25-OCT-2001; 2
08-FEB-2002; 2
06-MAR-2002; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU43663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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the invention fraction to an isolated minister actual comparisons of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
concleic acid; (2) a host cell containing the vector; (3) an isolated
colypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide of its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide of its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide of its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide of producing the polypeptide; (6) inhibiting cellular
corportiseration; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
corporated for proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits product lies
or againsm acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
compound's activity; (11) a culture comprising strains in which the gene
corporates or (13) identifying the target of a compound that inhibits the
corporation of an organism. The antisense nucleic acids are useful for
corporatined for proliferation in cells other than S. aureus, S. typhimurlum,
corporated prokaryotic essential genes. Note: The sequence data for this
confidential and product of the parined specification, but was obtained
in electronic format directly from WIPO at
                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of
                                                Zyskind JW;
Xu HH;
                                                Ohlsen KL,
Forsyth RA,
                                                Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 71587; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                Malone C,
Carr GJ,
                                                   Malone
(ELIT-) ELITRA PHARM INC.
                                                Zamudio C,
Trawick JD,
                                                                                                                            WPI; 2003-029926/02.
N-PSDB; ACA47533.
                                                   Wang L,
Wall D,
  %XCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCX
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Sequence 625 AA;

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5
                                                                     ------43 43
                               31; Gaps
          DB 6; Length 625;
                              31; Indels
                                                                                                               44 VNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQ 84
                   ilarity 21.8%; Pred. No. 33;
Conservative 17; Mismatches
           13.3%; Score 73.5;
                                                       8 RLKKKAQYEANKVKLWGLNTEYDNLLF---
Query Match
Best Local Similarity 21
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ADS30054 standard; protein; 1104 AA. ADS30054; RESULT 12 ADS30054 **EXXXXXXXXX**

02-DEC-2004 (first entry)

Bacterial polypeptide #19087.

Recombinant DNA construct, transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

RESULT 13

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a cransformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant comprising the recombinant DNA construct and growing the transforming a plant with the recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress production. This sequence represents a bacterial polypeptide used in the conduction. This sequence represents a bacterial polypeptide used in the form intend specification but was obtained in electronic format from intend a pecification or harman the form intend specification or harman the printed specification or man and the form intends the sequence when the man and the sequence when the conduction when the printed specification and the printed specification or harman harman the form intends and the sequence when the sequence when the conduction in the sequence when the conduction is the printed specification or the sequence when the conduction is the printed specification or provided plant in the sequence when the conduction is the printe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 GINTEYDNLIFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVA----- 75
pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; Length 1104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 GYTLDEIRNDITKKTPASFEPTIDYVVTKVP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQT-SEFVNQVLEKT-AEGNPTGGLVGLRIP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.3%; Score 73.5; D 27.5%; Pred. No. 68; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 19087; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cao Y, Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                                                                                                                        21-FEB-2002; 2002US-0360039P.
                                                                                                                                                                                                                                                                                           20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 27.5 ies 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-061375/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHEN X.
GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                                                           HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1104 AA;
                                                                                                                                                                                              US2003233675-A1.
                                                                                                                                                                                                                                           18-DEC-2003.
                                                                                                                                                 Bacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                       CAOY/)
                                                                                                                                                                                                                                                                                                                                                                                                                (HINK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                         (SLAT/)
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       ,8
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RESULT 14
                                                               ADN04305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A novel receptor interacting factor (AAW18226) is designated SWRT, i.e. silencing mediator (Go-repressor) for retinoic acid receptor (RAR) and thyroid hormone receptor (TR). Its association with RAR and TR both in solution and on DNA response elements is destabilised by ligand. The interaction of SMRT with mutant receptors correlates with the transcriptional silencing activities of receptors. In vivo. SMRT unctions as a potent co-repressor. A GAL4 DNA binding domain fusion of SMRT behaves as a frank repressor of a GAL4-dependent reporter. These data identify a novel class of cofactor which is believed to repersent an important mediator of hormone action. Full-length cDNA for SMRT has been isolated from a HeLa library in a two-hybrid screen using a GAL4 DNA binding domain/RXR fusion protein as bait
                                                                                               for retinoic acid and thyroid hormone receptor; SMRT;
                                                                                                                                                                                                                                                                                   1330. 1376
/note= "alternatively spliced insert not present in the original two-hybrid clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New co-suppressor of steroid-thyroid hormone receptor activity - also methods for identifying compounds that relieve its suppressant effect and/or activate receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.3%; Score 73.5; DB 2; Length 1495; 30.6%; Pred. No. 1e+02; tive 14; Mismatches 17; Indels 19.
                                                                                                                                                                                                                                  label= SG region
061. .1132
label= glutamine-rich region
                                                                                                                                                                                     'note= "proline-rich domain"
                                                                                                                                                                                                                                                                  1201. .1495
/label= C-terminal_region
                                                                                                                                                                               region
                                                                                                                                                                                                                                                                                                                                                                                                                     (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 40-45; 71pp; English.
               AAW18226 standard; protein; 1495 AA
                                                                                                                                                                                                 773. .790
/label= ERDR_region
                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                     . .160
label= N-terminal_
                                                                               Transcriptional co-repressor SMRT.
                                                                                                                                                                                                                                                                                                                                                                           96WO-US012371
                                                                                                                                                                                                                                                                                                                                                                                                 95US-00522726
                                                                                                     Silencing mediator for retine
transcriptional co-repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 30.69
Matches 22; Conservative
                                                                                                                                                                                                                         .827
                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-192894/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1495 AA;
                                                                                                                                                                                                                                                                                                                                                                              24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-1995;
                                                                                                                                                                                                                                                                                                                                     WO9709418-A1
                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        13-MAR-1997
                                                           24-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                             Evans RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                       AAW18226
                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                       Region
                                                                                                                                                                                                      Region
                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                      Region
         AAW18226
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-----PESLGVPTAQEAS-----VLRGTALGSVPG 1205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; SMRTe; nuclear receptor corepressor; gene therapy; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel polynucleotide and polypeptides for treating psoriasis or a sequence having at least 80% identity to the above sequences. The nucleic acid is useful for preparing a composition for diagnosing or treating psoriasis in a mammal. This sequence corresponds to one of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New PRO nucleic acid or polypeptide, useful for preparing a
pharmaceutical composition for diagnosing or treating psoriasis in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schoenfeld J, Williams PM,
                                                                                                                                                                                                                                                                                                   antipsoriatic; gene therapy; psoriasis; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.6%; Pred. No. 1.5e+02;
Matches 22; Conservative 14; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human nuclear receptor corepressor SMRTe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; SEQ ID NO 699; 3069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU61812 standard; protein; 2507 AA.
                                                                                                                                                                                                                                                               Antipsoriatic protein sequence #347.
                                                                                                                                         ADN04305 standard; protein; 2000 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jackman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1165 SGVKQEQL----SPRGQAGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-2003; 2003WO-US030907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2002; 2002US-0414006P
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|GSITKGIPSTRV 1217
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                         | : ||:::|
184 GSITKGIPSTRV 195
                                                                                                                                                                                                                           (first entry)
97 GLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-305105/28.
N-PSDB; ADN04304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2000 AA;
                                                                                                                                                                                                                                                                                                                                                                                            WO2004028479-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-AUG-2003
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                           01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bodary S,
Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1206
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                                                                                                                                                                                       ADN04305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammal.
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ABU61812
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3;

143

8 g,-

37 NSIKOBIVNRVONPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG

96

cancer

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The invention relates to an isolated SWRTe nucleic acid molecule. The nucleic acids are useful in gene therapy, as hybridisation probes for identifying SWRTe-encoding nucleic acid molecules and as primers for amplifying of SWRTe nucleic acid molecules and as primers for useful as immunogens to raise anti-SWRTe antibodies. The polypeptides are useful as targets for discovering and developing modulating agents to regulate a variety of cellular processes, in screening assays, in predictive medicine, in therapeutic or prophylactic treatment, in chromosome mapping, tissue typing and in forensic identification of a biological sample. Modulators of SWRTe are useful for treating or preventing a condition associated with aberrant SWRTe protein or nucleic acid expression or activity, such as cancer. The present sequence represents the amino acid sequence of the human nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New SMRTe proteins and nucleic acids, useful in gene therapy, predictive medicine, therapeutic or prophylactic treatment, chromosome mapping, tissue typing and in forensic biology.
                                                                                                          166 .206
/label= Amphipathic_helix
/noce= "Residues 172, 179, 186, 194 and 200 make up the
hydrophobic heptad repeat"
                                                                                                                                                                     130. .486
/label= SANT_A_domain
                                                                                                                                                                                                   613. .669 _ _ /label= SANT_B_domain
                                                            Location/Qualifiers
                                                                                          SNC_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                                  27-MAR-2001; 2001US-00819104.
                                                                                                                                                                                                                                                                                                                                                29-MAR-2000; 2000US-0193138P
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N-PSDB; ACA62249, ACA62250.
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                               Homo sapiens.
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                                                                             Domain
                                                                                                            Region
                                                                                                                                                                        Domain
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13.3%; Score 73.5; DB 6; Length 2507; 30.6%; Pred. No. 2e+02; tive 14; Mismatches 17; Indels 19; Gaps Query Match 13.3 Best Local Similarity 30.6 Matches 22; Conservative

37 NSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG 96

97 GLVGLRIPTSKV 108

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Search completed: February 28, 2006, 08:45:11 Job time : 39.9925 secs

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Sequence 41799, A
Sequence 570411 A
Sequence 1, Appli
Sequence 3809, Ap
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                                                                                                                                                            February 28, 2006, 08:53:26; Search time 9.29323 Seconds
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551
1 KLAFRACKLKKKKAQYEANKV......TABGNPTGGLVGLRIPTSKV 108
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                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
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US-09-328-352-210-1368

US-09-914-375C-26

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US-09-248-796A-22834

US-09-248-796A-22834

US-09-248-796A-22834

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US-09-248-76A-20333

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US-09-252-991A-16967
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Listing first 45 summaries
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Match Length DB
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 41799
LENGTH: 141
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Patent No. 6657054
GENERAL INFORMATION:
APPLICANT: Origene Technologies, Inc.
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT FILING DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE PATENTING DATE: 2002-06-10
SOFTWARE PATENTING DATE: 2002-06-10
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US-09-902-540-11503
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US-08-742-026-2
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100.0%; Score 551; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.3e-60;
Matches 108; Conservative 0; Mismatches 0;
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; Sequence 41799, Application US/09270767
; Patent No. 6703491
; GRNERAL INFORMATION:
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ORGANISM: Drosophila melanogaster
     TYPE: PRT
ORGANISM: Homo sapiens
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REFERENCE/DOCKET NUMBER: P41 90042
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                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 57041
LENGTH: 141
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Sequence 1, InfoRwariow.
Patent No. 6489441
InfoRwariow.
APPLICANT: Evans, Ponald M.
APPLICANT: Chen, J. Don
ITILE OF INVENTION: INTEREFOR
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36.7%; Score 202; DB 2; Length 141;
Best Local Similarity 43.6%; Pred. No. 2.2e-17;
Matches 48; Conservative 17; Mismatches 31; Indels
                                31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,726B
FILING DATE: 01-SEP-1995
           l Similarity 43.6%; Pred. No. 2.2e-17; 48; Conservative 17; Mismatches 31
                                                                                                                                                                                                                                                                                                                      Sequence 57041, Application US/09270767
Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Drosophila melanogaster US-09-270-767-57041
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NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
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MEDIUM TYPE: Floppy
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                Best Local Similarity
Matches 48; Conserv
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                                                                                                                                                                                                                                                                                 RESULT 3
US-09-270-767-57041
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TRANSCRIPTIONAL CO-REPRESSOR THAT INTERACTS WITH NUCLEAR HORMONI RECEPTORS
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Sequence 3809, Application US/09583110

Patent No. 6699703

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
ITILE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REPERENCE: PATHO0-079

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 SGVKQEQL----SPRCQAGP-----PESLGVPTAQEAS-----VLRGTALGSVPG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37 NSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG
                                                                                                                                                                                                                                                                                                                                                                                                        37 NSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                          17; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.3%; Score 73.5; DB 2; Length 1495; 30.6%; Pred. No. 9.1; .ive 14; Mismatches 17; Indels 19
                                                                                                                                                                                                                                                                                                          Length 1495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES APPLICANT: THE SALK RONALD APPLICANT: CHEN', J. TITLE OF INVENTION: TREEPTORS FILE OF INVENTION: RECEPTORS FILE REFERENCE: SALK1510-2 CURRENT APPLICATION UNMBER: US/09/337,384
CURRENT APPLICATION UNMBER: US/09/337,384
PRIOR APPLICATION NUMBER: 08/522,726
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 30.6%; Pred. No. 9.1;
Matches 22; Conservative 14; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 SGVKOEQL----SPRGOAGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-337-384-1
; Sequence 1, Application US/09337384
; Patent No. 6551773
; GENERAL INFORMATION:

man alik INSTITUTE FOR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
TELEPAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1495 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 08/5:
PRIOR FLING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.39
Best Local Similarity 30.69
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 GLVGLRIPTSKV 108
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184 GSITKGIPSTRV 195
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184 GSITKGIPSTRV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 GLVGLRIPTSKV 108
                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: both
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-583-110-3809
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LENGTH: 1495
                                                                                                                                                                                                                                                               US-08-522-726B-1
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OTHER INFORMATION: ENPL HUMAN ENDOPLASMIN PRECURSOR (94 KD GLUCOSE- REGULA)
                                                                                                                                                                                                                                  || ::| || : | || 520 LWEIDTSYDGI-----EIID-----ADNRDQSVLSFIRKGKKGEMLVCIFNMVPVE 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 DKIRLISLTDE--NAL---SGNEELTVKIKCDKEKNLLHVTDTGVGMTREELVKN-LGT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 NKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDER-----GPNMGQKLEILIKDTLGL
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                        22 LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM-----GQKLEILI---
                                                                                                                                                           Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Steven A, Benner
Applications of Protein Structure Predictions
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS: 74
ADDRESSEE: Steven A. Benner
STREET: 1501 NW 68th Terrace
CITY: Gainesville
                                                                                                                 Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IndelB
                                                                                                            ; Score 72.5; DB 2;
; Pred. No. 3.7;
12; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 12.5%; Score 69; DB 2;
Best Local Similarity 27.3%; Pred. No. 2.3;
Matches 24; Conservative 19; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States
ZIP: 32605-4147
COMPUTER READABLE FORM:
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,375C
NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...651
SEQUENCE DESCRIPTION: SEQ ID NO: 2845:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 PVAGQISEFVNQVLEKTAEGNPIGGLVG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 IAKSGTSEFLNKMTEAQEDĞQSTSELIG 123
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SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                           566 RKDFTIGLPVAGIYEEVWNTELEE 589
                                                                                                                                                                                                                                                                                                    67 -KD-TLGLPVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-914-375C-25; Application US/08914375C; Sequence 25; Application US/08914375C; Patent No. 6377893; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-Aug-1997
CLASSIFICATION: 702/20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 352 392 7773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 352 331 0462 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: amino acid
ORIGINAL SOURCE:
                                                                                                              Query Match 13.2%;
Best Local Similarity 31.0%;
Matches 26; Conservative 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: FL
                                                        ;
US-09-107-433-2845
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                 Query Match 13.2%; Score 72.5; DB 2; Length 642; Best Local Similarity 31.0%; Pred. No. 3.7; Matches 26; Conservative 12; Mismatches 15; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                             22 LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM-----GQXLEILI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: <URNOWN>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Unn-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                     PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
LENGTH: 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
       US 09/107,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02354
UTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 -KD-TLGLPVAGQTSEFVNQVLEK 88
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OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2845, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2845:
                                                                                                                                                                                                                                  ORGANISM: Streptococcus pneumoniae US-09-583-110-3809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 651 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
       PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-107-433-2845
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Applications of Protein Structure Predictions
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MEDIUM TYPE: 3.5 inch diskette
COMPUTER: 3.5 inch diskette
COMPUTER: 4pple MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,375C
FILING DATE: 19-Aug-1997
CLASSIFICATION: 702/20
TELECOMMUNICATION: 702/20
TELEFAX: 352 392 7773
TELEFAX: 352 331 0462
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                              CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
STREET: 1501 NW 68th Terrace
CITY: Gainesville
                                                                                                                                                                                 COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 GOSTSELIG 123
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                    Sequence 5821, Application US/09328352

Batent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBENCE: GT-99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

MUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----M 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
12.3%; Score 67.5; DB 2; Length 150;
Best Local Similarity 29.4%; Pred. No. 2;
Matches 30; Conservative 11; Mismatches 32; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: ALL'I-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-71(15036)
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR PILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
12.3%; Score 68; DB 2; Length 2504;
Best Local Similarity 26.6%; Pred. No. 93;
Matches 25; Conservative 10; Mismatches 31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1731 GEKLNIIGGAAASTPVAKTSGE--NVITRTTQDG 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 LNTEYDNLLFVINSIKQEIVNRVQNPRDE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1368, Application US/09732210
Patent No. 6573361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORCANISM: Methanococcus jannaschii
US-09-732-210-1368
                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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US-08-914-375C-24
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OTHER INFORMATION: ENPL_CANFA ENDOPLASMIN PRECURSOR (94 KD GLUCOSE- REGULA)
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                                                                                                                                                                                                                                                                                                                                                                                    5 KFARQA------EVNRMMKLIINSLYKNKEIFLRELISNASDALDKIRLISLTDENA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                        40 ---KQEIVNRVQNPRDER-----GPNMGOKLEILIKDTLGLPVAGQTSEFVNQVLEKTAE 91
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENUELO S. Application US/08914375C
Patent No. 6377893
GENERAL INFORMATION:
APPLICANT: Steven A. Benner
Applications of Protein Structure Predictions
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSE: Steven A. Benner
ADDRESSE: Steven A. Benner
CITY: Gainesville
CITY: Gainesville
                                                                                                                                                                                                                                              Length 223;
                                                                                                                                                                                                                                                                                          41; Indels
                                                                                                                                                                                                                                                                                                                                             1 KLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSI
                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                              Query Match 12.3%; Score 67.5; Di
Best Local Similarity 20.2%; Pred. No. 3.5;
Matches 26; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 32605-4147
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh
SOFTWARE: Microsoft Word
                                                                                                                              PROTEIN) (GRP94)
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-914-375C-24
TOPOLOGY: linear
MOLECULE TYPE: amino acid
ORIGINAL SOURCE:
ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: United States
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Sequence 24, Application US/08914375C Patent No. 6377893

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GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: 0.860/074,725
FRIOR APPLICATION NUMBER: US 60/074,725
FRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEG ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 RLKKKAQYEANKVKLWGLN---TEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQKLEI 64
                                                                                                                      APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Oskar
APPLICANT: Schroder, Oskar
APPLICANT: Alberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
TITLE OF INVENTION: PROTEINS
FILE REPERENCE: BG1-12GP
CURRENT FILING DATE: 2000-06-27
CURRENT APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2934
SEQ ID NOS: 2934
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12.1%; Score 66.5; DB 2; Length 356;
Best Local Similarity 21.1%; Pred. No. 9.1;
Matches 19; Conservative 19; Mismatches 31; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 12.2%; Score 67; DB 2; Length 481; 1 Similarity 22.8%; Pred. No. 12; 21; Conservative 21; Mismatcher 74. Teach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 LIKDT---LGLP-----VAGQTSEFVNQVL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 GPNMGOKLEILIKDTLGLPVAGQTSEFVNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-248-796A-22834
; Sequence 22834, Application US/09248796A
; Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 AQYEANKVKLW----GLNTEYDNLLF---
                                   Sequence 2774, Application US/09605703B Patent No. 6962989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Corynebacterium glutamicum
                                                                                                        APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-248-796A-22834
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PILE REFERENCE: 107196.132
PRIOR PELLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: ENPL MOUSE ENDOPLASMIN, PRECURSOR (94 KD GLUCOSE- P11427 (98-914-375C-26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 KFARQA------EVNRWMKLIINSLYKNKEIFLRELISNASDALDKIRLISLIDENA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 ---KQEIVNRVQNPRDER-----GPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- GPNMGQKLEILIKDTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.3%; Score 67.5; DB 2; Length 223; 20.2%; Pred. No. 3.5; tive 23; Mismatches 41; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 LNTE-YD--NLLFVINSI----KQEIVNRVQNPRDER---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67.5; DB 2;
Pred. No. 20;
3; Mismatches 23;
                  APPLICATION NUMBER: US/08/914,375C
FILING DATE: 19-Aug-1997
CLASSIFICATION: 702/20
TELECOMMUNICATION INFORMATION:
TELEFAX: 352 392 7773
TELEFAX: 352 331 0462
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 LPVAGQTSEFVNQVLEKTAE-GNPTGGLVG 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Mus musculus
                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: amino acid
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Conservative
                                                                                                                                                                                                                                TYPE: amino acid
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Best Local Similarity
Matches 26; Conserva
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Best Local Similarity
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Search completed: February 28, 2006, 08:56:08 Job time : 9.54323 secs

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RESULT 2
US-11-097-143-31914
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3509, Ap
Sequence 23307, A
Sequence 8932, Ap
Sequence 6933, Ap
Sequence 5251, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44, Appl
Sequence 31914, A
Sequence 59634, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3265, Ap
Sequence 12, Appl
                                                                                  February 28, 2006, 08:54:36; Search time 31.4887 Seconds (without alignments) 1433.071 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                  US-10-717-665A-44_COPY_532_639
551
1 KLAFRACRLKKKKAQYEANKV......TABGNPTGGLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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Sequence
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                                                                                                                                                                                                                                                                                                                                                         Published Applications_AA_Main:*

(gqn2_6/ptodata/1/pubpa/USO2_PUBCOMB.pep:*

(gqn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

(gqn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

(gqn2_6/ptodata/1/pubpaa/USO3_PUBCOMB.pep:*

(gqn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

(gqn2_6/ptodata/1/pubpaa/USII_PUBCOMB.pep:*
            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-717-665-44
US-11-097-13-31914
US-11-097-13-31914
US-10-282-122A-47201
US-10-369-493-1968
US-10-369-493-1968
US-10-369-493-1968
US-10-369-493-1968
US-10-369-493-1968
US-10-369-493-1968
US-10-705-165-26
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US-10-369-493-5251
US-10-369-493-5251
US-10-369-493-5251
US-10-369-493-5251
                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                     1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            - protein search, using sw model
                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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                                                                                                                                                                                                                        Searched:
                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                              Database
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Sequence 31914, Application US/11097143
; Sequence 31914, Application No. US200S02085S8A1
; Publication No. US200S02085S8A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: DROSOPHILA GENES.
; TITLE OF INVENTION: DROSOPHILA GENES.
; TITLE OF INVENTION: DROSOPHILA GENES.
; GURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-19
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74571
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4, Appli
4, Appli
5897, App
8103, Ap
2706, Ap
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; Sequence 44, Application US/10717665
; Publication Wo. US20050106579A1
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies, Inc.
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
; CURRENT APPLICATION NUMBER: US/10/717,665
; PRIOR APPLICATION NUMBER: US/10/164,595
; PRIOR FILING DATE: 2002-10-10
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 639
; TYPE: PRT
; ORGANICM: Home Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 514,
Sequence 79,
Sequence 78,
Sequence 2,
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Sequence
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US-10-369-493-2816
US-10-415-868-2
US-10-282-128-74571
US-09-968-4368-4
US-10-260-1048-4
US-10-260-1048-4
US-10-369-493-8103
US-10-369-493-8103
US-10-264-049-2706
US-09-759-010-7
US-10-264-048-2106
US-09-759-010-7
US-10-264-048-2
US-10-231-553-3
US-10-260-1048-2
US-10-260-1048-2
US-10-260-1048-2
US-10-260-1048-2
US-10-260-1048-2
US-10-260-1048-2
US-10-789-378-78
US-10-789-378-78
US-10-789-378-78
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100.0%; Pred. No. 3.4e-54;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 108; Conservative
            1105
220
282
282
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Publication No. US20040029129A1
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Matches 24; Conserva
                       GENERAL INFORMATION:
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US-10-472-928-2234
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                       36.7%; Score 202; DB 6; Length 814; 43.6%; Pred. No. 6.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 59634, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyeeq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES; FILE REFERENCE: 790C1P3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-66-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR PLING DATE: 2000-03-31
; PRIOR PLING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17; Mismatches
                                          PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR PLING DATE: 1999-12-18
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PELING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/194,831
PRIOR PELING DATE: 2000-02-24
PRIOR PELING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-33
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FREESEQ for Windows Version 4.0
      APPLICATION NUMBER: 60/161,932
FILING DATE: 1999-10-28
APPLICATION NUMBER: 60/164,769
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.7%
Best Local Similarity 43.6%
Matches 48; Conservative
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SOFTWARE: Custom
SEQ ID NO 59634
LENGTH: 160
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US-10-450-763-59634
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Matches 46; Conserv
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US-10-450-763-59634
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                                                                                                                                                                                                                                                                                               SEQ ID NO 31914
LENGTH: 814
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US-10-282-122A-47201

RESULT 4

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APPLICANIT: Xu, H.

APPLICANIT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA.0340
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/200,335
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
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Publication No. US20050020813A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
FILE REFERENCE: P026926WO
CURRENT APPLICATION NUMBER: US/10/472,928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: GB-0107658.7
PRIOR FILING DATE: 2001-03-27
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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US-10-282-122A-47201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 PVAGQTSEFVNQVLEK 88
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REPERENCE: 38-10 (52052)8 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374 EDGITH OF 19968 LENGTH: 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.5%; Score 74.5; DB 4; Length 1124; Best Local Similarity 28.6%; Pred. No. 48; Matches 26; Conservative 11; Mismatches 37; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 GLNTEYDNILFVINSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVA-
                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)..(1124); OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-19968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQT-SEFVNQVLEKT-AEGNPIGGLVGLRIP 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: No. US20030233675Altoc punctiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 71587, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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Forsyth, R.
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
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Wall, Daniel
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Carr, Grant
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NAME/KEY: unsure
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR PILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22667
LENGTH: 1175
                                                                                                                                                                                                                                                                                                                                  2 LAFRACRLKKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 VCLNSCRFYNETRSQLREKRFFVGXNLYINILFLISNVKRIRASRNQDNRPERQSRL-QR 96
                                                                                                                                                                                                                                                                                                            9 LKKKAQYEANKVK-----LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM--
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                                                                                                                                                                                                                        DB 5; Length 345;
                                                                                                                                                             , OTHER INFORMATION: 1,4-alpha-glucan branching enzyme-related
US-10-472-928-2234
                                                                                                                                                                                                                                                                                                                                                                                                                      239 FIRKGKKGEMLVCIFNMVPVERKDFTIGLPVAGIYEEVWNTELEE 283
                                                                                                                                                                                                                                                                                                                                                                                            59 ----GQKLEILI-----KD-TLGLPVAGQTSEFVNQVLEK 88
                                                                                                                                                                                                                                                                20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(1175)
CTHER INFORMATION: unsure at all Xaa locations US-10-369-493-22667
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                                                                                                                                                                                                                        Query Match
13.7%; Score 75.5; Di
Best Local Similarity 27.6%; Pred. No. 7.6;
Matches 29; Conservative 17; Mismatches
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; Sequence 19968, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22667, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Schizosaccharomyces pombe
                                                                                               TYPE: PRT ORGANISM: Streptococcus pneumoniae
             SEQ ID NOS: 4979
SegWin99, version 1.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Conservative
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Best Local Similarity
Matches 23; Conserv
           NUMBER OF SEQ ID N
SOFTWARE: SegWin99
SEQ ID NO 2234
LENGTH: 345
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                                                                                                                                         FEATURE:
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Gaps

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APPLICANT: Hur, Eugene
APPLICANT: Bucher, Ben
TITLE OF INVENTION: Inhibitors for Androgen Antagonist Refractory Prostate Cancer;
FILE REFERENCE: 061040-0018-US
CURRENT APPLICATION NUMBER: US/10/705,165
CURRENT APPLICATION NUMBER: US 60/29,956
PRIOR APPLICATION NUMBER: US 60/079,956
PRIOR PILING DATE: 1998-03-30
PRIOR PLING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: US 60/113,146
PRIOR PLING DATE: 1998-12-16
PRIOR APPLICATION NUMBER: US 99/69,361
PRIOR APPLICATION NUMBER: US 09/69,361
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PELING DATE: 1999-130
PRIOR PILING DATE: 1999-13-30
PRIOR PILING DATE: 1999-13-30
PRIOR SPELICATION NUMBER: US 60/113,014
PRIOR SPELICATION NUMBER: US 60/113,014
PRIOR PILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 NSIKQEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                  Ouery Match
13.3%; Score 73.5; DB 4; Length 1495;
Best Local Similarity 30.6%; Pred. No. 91;
Matches 22; Conservative 14; Mismatches 17; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%; Score 73.5; DB 5; Length 1495; 30.6%; Pred. No. 91;
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            CURRENT APPLICATION NUMBER: US/10/351,750
CURRENT FILING DATE: 2003-01-23
PRIOR APPLICATION NUMBER: US/09/337,384
PRIOR FILING DATE: 1999-06-21
PRIOR PLING DATE: 1995-09-01
PRIOR PLING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/10705165 Publication No. US20050202440A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fletterick, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 GLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 GLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 GSITKGIPSTRV 195
FILE REFERENCE: SALK1510-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-705-165-26
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                                                                                                                                                                                                                                            LENGTH: 1495
                                                                                                                                                                                                                                                                                                               US-10-351-750-1
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                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                   SEQ ID NO 1
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| Publication No. US20030138836A1
| GENERAL INFORMATION:
| APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
| APPLICANT: EVANS, RONALD
| APPLICANT: CHEN, J.
| TITLE OF INVENTION: RECEPTORS
| TITLE OF INVENTION: RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeen
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52.052)8
FILE REPERENCE: 38-10(52.052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19087
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                                                                                                                                                                                                                                                                                                                                                                   31; Gaps
  Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 71587
LENGTH: 625
TYPE: PRT
ORGANISM: Staphylococcus haemolyticus
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27.5%; Pred. No. 61;
tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                          8 RLKKKAQYEANKVKLWGLNTEYDNLLF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19087, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                               NAME/KEY: MISC FEATURE
LOCATION: (608)
COTHER INFORMATION: X=any amino acid
US-10-282-122A-71587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Anabaena PCC7120
US-10-369-493-19087
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Best Local Similarity 27.55
Matches 25; Conservative
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                                                                                                                                                                                   FEATURE:
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Publication No. US20020182586A1
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Matches 22; Conserva
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Glothik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions of TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 13.3%; Score 73.5; DB 3; Length 2507; Best Local Similarity 30.6%; Pred. No. 1.8e+02; Matches 22; Conservative 14; Mismatches 17; Indels 19; Gaps
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                               ; Sequence 2, Application US/09819104A; Bublication No. US20030027137A1; GENERAL INFORMATION:
; APPLICANT: Chen, J. Don
; TITLE OF INVENTION: NOVEL NUCLEAR RECEPTOR COREPRESSOR MOLECULES; FILE REFERENCE: UMG-030
; CURRENT APPLICATION NUMBER: US/09/819,104A
; CURRENT PILING DATE: 2001-03-27; PRIOR APPLICATION NUMBER: 60/193,138
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 6
; SOFFWARE: Patentin Ver. 2.0
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; Sequence 1740, Application US/10723860
; Publication No. US20040253606Al
; GENERAL INFORMATION:
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US-10-087-192-654
; Sequence 654, Application US/10087192
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 1740
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Best Local Similarity 30....
Best Local Scholarity 30....
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1196 GSITKGIPSTRV 1207
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1196 GSITKGIPSTRV 1207
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CRGANISM: Homo sapiens
US-10-723-860-1740
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 2507
                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-819-104A-2
                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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FOR DIAGNOS
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US-10-20-2845
US-10-617-320-2845,
Sequence 2845, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: PRELATING TO STREPTOCOCCUS PNEUMONIAE
; TITLE OF INVENTION: DAVID AMINO ACID
; TITLE OF INVENTION: DAVID AMINO ACID
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
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; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
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GENERAL INVORMATION:
APPLICANT: MOTELS, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 5.2945200122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-103-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
TYPE: PRT
TYPE: PRT
TYPE: PRT
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: uS/10/617,320
FILING DATE: 10-Jul-2003
PRIOR APPLICATION NUMBER: US/09/107,433
APPLICATION NUMBER: US/09/107,433
APPLICATION NUMBER: 60/085131
FILING DATE: MAy 12, 1998
APPLICATION NUMBER: 60/05153
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
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COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
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STATE: Massachusetts
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COMPUTER READABLE FORM:
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TELEFAX: (781)893-827

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| INPORMATION POR SEQ ID NO: 2845:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 631 amino acida | TYPE: amino acida | TYPE: amino acida | TYPE: amino acida | TYPE: amino acida | TYPE: amino acida | TYPE: amino acida | TYPE: amino acida | TYPE: amino acida | TYPE: amino acida | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein | TYPE: protein |
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TYPE: PRT
CORGANISM: Homo sapiens
US-10-821-234-1643
US-10-962-951-2
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Sequence 1269, Ap
                                                                                                                                                                       (without alignments)
556.876 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                   February 28, 2006, 08:56:26; Search time 2.88722 Seconds
                                                                                                                                                                                                                                                                                  1 KLAFRACRLKKKAQYEANKV......TAEGNPTGGLVGLRIPTSKV 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA New:*

1: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
                      GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-962-951-2

US-10-812-234-901

US-10-87-556A-136

US-10-467-657-314

US-11-087-719-15

US-11-087-719-14

US-11-087-719-14

US-11-087-719-14

US-11-087-719-14

US-11-057-626A-34

US-11-055-822-306

US-11-055-822-306

US-11-055-822-306

US-11-055-822-1002

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US-11-055-822-1002

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US-11-055-822-115

US-11-052-951-17
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551
                                                                                                                                                                                                                                                                                                                                                                                          117670 segs, 14887254 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                          protein search, using sw model
                                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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                                                                                                            OM protein
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26 61 11.1 333 6 US-10-821-234-1323 Sequence 1323, Appl 27 61 11.1 333 6 US-10-870-556A-85 Sequence 13.7 Appl 28 60 10.9 504 7 US-11-121-438-6 Sequence 17.0 Appl 30 59 10.7 509 7 US-11-024-959-393 Sequence 17.0 Appl 31 59 10.7 509 7 US-11-024-959-393 Sequence 2. Appl 33 59 10.7 831 7 US-11-108-746-5 Sequence 5. Appl 33 58.5 10.6 281 7 US-11-128-43-180 Sequence 5. Appl 36 58.5 10.6 281 7 US-11-122-443-180 Sequence 5. Appl 36 58.5 10.6 281 7 US-11-212-443-180 Sequence 5. Appl 36 58.5 10.6 284 7 US-11-212-443-180 Sequence 5. Appl 37 58.5 10.6 284 7 US-11-212-443-180 Sequence 19. Appl 39 58.5 10.6 1574 7 US-11-212-443-179 Sequence 19. Appl 40 58 10.5 310 7 US-11-212-443-60 Sequence 6.0 Appl 40 58 10.5 310 7 US-11-212-443-60 Sequence 6.0 Appl 40 58 10.5 310 7 US-11-212-443-60 Sequence 5. Appl 40 58 10.5 310 7 US-11-212-443-60 Sequence 5. Appl 40 58 10.5 310 7 US-11-212-443-60 Sequence 5. Appl 40 58 10.5 310 7 US-11-212-443-60 Sequence 5. Appl 41 58 10.5 310 7 US-11-212-46 Sequence 5. Appl 41 58 10.5 310 7 US-11-212-46 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-212-46 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-196-71-60-5 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-196-71-60-5 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-196-71-60-5 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-196-71-60-5 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-196-71-60-5 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-196-71-60-5 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-196-71-60-5 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-196-71-60-5 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-196-71-60-5 Sequence 6.0 Appl 42 58 10.5 310 7 US-11-196-71-60-5 Sequence 8.0 Appl 42 58 10.5 310 7 US-11-198-71-60-5 Sequence 8.0 Appl 42 58 10.5 310 7 US-11-198-71-60-5 Sequence 8.0 Appl 42 58 10.5 310 7 US-11-198-71-60-5 Sequence 8.0 Appl 42 58 10.5 310 7 US-11-198-71-60-5 Sequence 8.0 Appl 42 58 10.5 310 7 US-11-198-71-60-5 Sequence 8.0 Appl 42 58 10.5 800 Sequence 8.0 Appl 42 58 10.5 800 Sequence 8.0 Appl 42 58 10.5 800 Sequence 8.0 Appl 42 58 10.5 800 Sequence 8.0 Appl 42 58 10.5 800 Sequence
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ALIGNMENTS

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RESULT 1

UB-10-81-234-1643

Sequence 1643, Application US/10821234

Sequence 1643, Application US/10821234

Sequence 1643, Application US/10821234

Sequence 1643, Application US/10821234

GENERAL INFORMATION:
APPLICANT: Laber, Ivan
APPLICANT: Abade, Ivan
APPLICANT: Abade, Ivan
APPLICANT: Abade, Ivan
APPLICANT: Abade, Ivan
APPLICANT: Abade, Ivan
APPLICANT: Abade, Ivan
APPLICANT: Abade, Ivan
APPLICANT: Abade, Ivan
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APPLICANT: Abade, Ivan
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APPLICANT: Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade, Abade,
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Sequence 3272, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
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SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 314
LENGTH: 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-467-657-3272
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US-10-467-657-314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-821-234-901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 NKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDER-----GPNMGQKLEILIKDTLGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 ONPRDERGPNMGOKLEILIKDTLGLPVAGQTSEFV-NOVLE-----KTAEGNPTGG 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.2%; Score 67; DB 6; Length 1410;
Best Local Similarity 33.9%; Pred. No. 26;
Matches 20; Conservative 9; Mismatches 14; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
12.5%; Score 69; DB 6; Length 803;
Best Local Similarity 27.3%; Pred. No. 7.3;
Matches 24; Conservative 19; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HCV regulated protein expression FILE OF INVENTION: HCV regulated protein expression FILE OF INVENTION: 2172 CURRENT PPPLICATION NUMBER: US/10/878,556A CURRENT FILING DATE: 2004-06-28 NUMBER OF SEQ ID NOS: 199
SOFTWARE: Patentin version 3.1
SEQ ID NO 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: amino acid sequence human GRP94 US-10-962-951-2
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ORGANIEM: Homo sapiens
PUBLICATION INFORMATION:
DUALABASE ACCESSION NUMBER: sw_hum/rrbl_human
DATABASE ENTRY DATE: 2003-02-28
                 TILLE REPERRICE: 3460-CHOP.C-206US
CURRENT APPLICATION NUMBER: US/10/962,951
CURRENT FILING DATE: 2004-10-12
RINGRAPHICATION NUMBER: US/10/844,711
PRIOR APPLICATION NUMBER: US/10/844,711
PRIOR PILING DATE: 2004-05-12
PRIOR PILING DATE: 2003-05-12
PRIOR PILING DATE: 2003-06-12
PRIOR PILING DATE: 2003-06-12
PRIOR PILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2004-04-28
PRIOR FILING DATE: 2004-04-28
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PRIOR PILING DATE: 2004-04-28
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TITLE OF INVENTION: USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Sequence 901, Application US/10821234 Publication No. US20050255114A1

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APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preclampsia
TITLE OF INVENTION: WOUNBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: DL SEQ genes Version 1.0
SEQ ID NOS: 1704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Indels 16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.2%; Score 67; DB 6; Length 1586; 33.9%; Pred. No. 30; tive 9; Mismatches 14; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
12.0%; Score 66; DB 6; Length 207;
Best Local Similarity 22.8%; Pred. No. 2.6;
Matches 26; Conservative 17; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHIRON SpA
APPLICANT: GUTRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REPRENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT PILING DATE: 2003-08-11
PRIOR FILING DATE: 2001-02-12
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APPLICANT: PONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
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APPLICANT: Ochiette, Benoit
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Alakhov, Valery
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR TREATING DISEASES THAT
TITLE OF INVENTION: INVOLVE ANGIOGENESIS
FILE REFERENCE: PO86051501/BAS
CURRENT APPLICATION NUMBER: 1201-24
FRIOR APPLICATION NUMBER: US 60/555,668
FRIOR FILING DATE: 2004.03-24
                   APPLICANT: Alakhov, Valery
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR TREATING DISEASES THAT
TITLE OF INVENTION: THERAPEUTIC COMPOSITIONS AND METHODS FOR TREATING DISEASES THAT
FILLE REFERENCE: P08605US01/BAS
CURRENT APPLICATION NUMBER: US/11/087,719
CURRENT FILLING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: US 60/555,668
PRIOR FILLING DATE: 2004-03-24
NUMBER OF SEC ID NOS: 88
SOFTWARE: Patentin version 3.3
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Publication No. US20050255114A1
Publication No. US20050255114A1
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Applicant, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LKKKAQYEANKVK--LWGLNTEYDNLLFVINS-IKQEI--VNRV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 LKKKAQYEANKVK--LWGLNTEYDNLLFVINS-IKQEI--VNRV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65.5;
Pred, No. 5.
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Pred. No. 5.
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CURRENT APPLICATION NUMBER: US/10/821,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/11087719
Publication No. US20050277575A1
GENERAL INFORMATION:
Grzegorz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Semov, Alexander
APPLICANT: Onichtchenko, Anatoli
APPLICANT: Iourtchenko, Ludmila
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 43.2%;
Matches 19; Conservative 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin version 3.3
SEQ ID NO 13
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Best Local Similarity 43.2%;
Matches 19; Conservative 1.
APPLICANT: Pietrzynski,
                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-11-087-719-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-087-719-13
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US-10-821-234-1507
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LENGTH: 323
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APPLICANT: Semov, Alexander
APPLICANT: Semov, Alexander
APPLICANT: Conictichenko, Ludmila
APPLICANT: Ochiette, Benoit
APPLICANT: Ochiette, Benoit
APPLICANT: Pietrzynski, Grzegorz
APPLICANT: Alakhov, Valery
TITLE OF INVENTION: THERAPETYIC COMPOSITIONS AND METHODS FOR TREATING DISEASES THAT
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TITLE OF INVENTION: THERAPETYIC COMPOSITION AND METHODS FOR TREATING DISEASES THAT
TITLE OF INVENTION: 1NVOLVE ANGIOGENESIS
FILE REPERENCE: POSSOGOUSOLIPAS
CURRENT APPLICATION NUMBER: US 60/555,668
PRIOR PILING DATE: 2004-013-24
RUMBER OF SEQ ID NOS: 88
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 GPNMGOKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 108
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                                                                                                                                                                                                                                                                                                                                                                                                                             12.0%; Score 66; DB 6; Length 207; 22.8%; Pred. No. 2.6; tive 17; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LKKKAQYEANKVK--LWGLNTEYDNLLFVINS-IKQEI--VNRV 47
                        APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 CRIKNVVWKTLGEVAEYSKNRICSDKINEHNYVGVDNLL---
                                                                                                 CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3272
LENGTH: 207
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Publication No. US20050277575A1
GENERAL INFORMATION:
APPLICANT: Semov, Alexander
APPLICANT: Onichtchenko, Anatoli
APPLICANT: Onichtchenko, Ludmila
APPLICANT: Ochiette, Benoit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/11087719
Publication No. US200502775751
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3272
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 22.8
Matches 26; Conservative
  APPLICANT: MASIGNANI Vega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCREMATION:
APPLICANT: POMPETAL WARKUS
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gregor
TITIE OF INVENTION: CORYNBARGTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNBARGTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNBARGTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNBARGTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNBARGTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNBARGTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNBARGTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION NUMBER: 60/140, 1031
PRIOR FILING DATE: 1999-00-62
PRIOR FILING DATE: 1999-00-02
PRIOR FILING DATE: 1999-00-03
PRIOR FILING DATE: 1999-00-03
PRIOR FILING DATE: 1999-00-03
PRIOR PAPLICATION NUMBER: DE 19931418.7
PRIOR APPLICATION NUMBER: DE 19931418.7
PRIOR PAPLICATION NUMBER: DE 19931418.7
PRIOR FILING DATE: 1999-00-08
PRIOR FILING DATE: 1999-00-08
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PRIOR FILING DATE: 1999-00-09
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PRIOR FILING DATE: 1999-00-09
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                                                                                                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: (237)...(237)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-207-626A-34
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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 25.3%; Pred. No. 6.7;
Matches 21; Conservative 17; Mismatches 34; Indels 1.
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11.9%; Score 65.5; Dl
1 Similarity 27.5%; Pred. No. 26;
25; Conservative 11; Mismatches
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 ERGPNMGOKLEILIKDTLGLPVA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 370, Application US/11055822 Publication No. US20050260707A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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LENGTH: 1066
TYPE: PRT
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Sequence 143, Application US/11072175

Publication No. US20060029944A1

Sequence 143, Application No. US2006002994A41

Sequence 143, Application No. US2006002994A41

Sequence 143, Application No. US2006002994A41

FUDICANT: BETSETCH-Myers Squibb Company

APPLICANT: BETSETCH-Myers Squibb Company

APPLICANT: DEATHER ADDICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT

TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR

TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS

CURRENT APPLICATION NUMBER: US 40406,385

PRIOR FILING DATE: 2002-08-26

NUMBER OF SEQ ID NOS: 571

SOFTWARE: Patentin version 3.2

SEQ ID NO 143

LEMOTH: 339

TYPE: PRI

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11.9%; Score 65.5; DB 7; Length 339;
Best Local Similarity 43.2%; Pred. No. 5.8;
Matches 19; Conservative 11; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
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Sequence 34, Application US/11207626A
Sequence 34, Application No. US20060014276A1
GENERAL INFORMATION:
APPLICANT: Havenga, Menzo
APPLICANT: Wogels, Ronald
APPLICANT: Bout, Abraham
TITLE OF INVENTION: CHIMERIC ADENOVIRUSES
FILER REFERENCE: 2578-4123.2US
CURRENT APPLICATION NUMBER: US/11/207,626A
CURRENT APPLICATION NUMBER: EP 98202297.2
PRIOR FILING DATE: 1998-07-08
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
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Best Local Similarity 43.2%; Pred. No. 5.8;
Matches 19; Conservative 11; Mismatches
              CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1507
LENGTH: 339
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US-11-072-175-143
                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-10-821-234-1507
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US-11-072-175-143
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Pompedilon:
APPLICANT: Except. Burkhard
APPLICANT: Schröder, Hartwig
APPLICANT: Schröder, Hartwig
APPLICANT: Schröder, Hartwig
APPLICANT: Calder, Oskar
APPLICANT: Calder, Oskar
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
TITLE OF INVENTION WHERE: US/11/055,822
CURRENT APPLICATION NUMBER: 05/66,740
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-12
PRIOR PILING DATE: 1999-08-12
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-01
PRIOR PILING DATE: 1999-07-08
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APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gostor
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
11.9%; Score 65.5; DB 7;
Best Local Similarity 27.5%; Pred. No. 26;
Matches 25; Conservative 11; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 | | | | : : | | | | : : | 287 GYTLDEITNDITGETPAAFEPTIDYVVVKAP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQT-SEFVNQVLEKT-AEGNPTGGLVGLRIP 104
76 GQT-SEFVNQVLEKT-AEGNPTGGLVGLRIP 104
                                                             287 GYTLDEITNDITGETPAAFEPTIDYVVVKAP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 1158
SEQ ID NO 1002
                                                                                                                                                                                                                             Sequence 1002, Application US/11055822
Publication No. US20050260707A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Corynebacterium glutamicum
US-11-055-822-1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 368, Application US/11055822 Publication No. US20050260707A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-11-055-822-368
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FILE REFRENCE: BGI-121CPCN WALTHOUS PAITHWAY PROTEINS
FILE REFRENCE: BGI-121CPCN US/11/055,822
CURRENT FILING DATE: 2005-02-11
PRIOR APPLICATION NUMBER: 00/141,031
PRIOR PLING DATE: 1999-06-25
PRIOR PLING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-07-02
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11.9%; Score 65.5; DB 7; Length 1113;
Best Local Similarity 27.5%; Pred. No. 28;
Matches 25; Conservative 11; Mismatches 38; Indels 17;
METABOLIC PATHWAY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 GOT-SEFVNOVLEKT-AEGNPTGGLVGLRIP 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 28, 2006, 09:02:41 Job time : 3.88722 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Corynebacterium glutamicum
US-11-055-822-368
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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28, 2006,		
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Run on:		

US-10-717-665A-44_COPY_532_639 551 1 KLAFRACKLKKKKAQYEANKV......TABGNPTGGLVGLRIPTSKV 108 Title: Perfect score: Sequence:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		two-component hybr	hypothetical prote	unknown protein T6	dimethyladenosine	hypothetical prote	1,4-alpha-glucan b	conserved hypothet	pps1 protein - Myc	carbamoyl phosphat	transcription co-r	inositol-3-phospha	2	related to SHK1 KI	H+-transporting tw	hypothetical prote	probable glycine-t	nicotinate-nucleot	hypothetical prote	carbamoyl-phosphat	conserved hypothet		hypothetical prote	endoplasmin precur			hypothetical prote	drought-induced pr	hyrin	ribosomal protein
	ΙD	1 1 1 1 1 1	AH2067	T00072	F96713	E70173	865157	G95129	A86983	872760	AB2282	S60255	T08436	E98000	T49572	JN0760	T22552	S48285	AD2116	H70871	876557	AH2712	F97494	F82338	A35954	C34233	E75588	T23171	S71561	AE2351	F64323
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	Query Match Length		571	902	534	281	455	642	869	869	1104	1495	509	642	718	505	1355	667	200	846	1105	315	315	330	803	222	386	552	258	1328	186
مد	Query Match		14.9	14.9	14.4	14.2	13.9	13.7	13.4	13.4	13.3	13.3	13.2	13.2	13.1	12.9	12.9	12.8	12.7	12.7	12.6	12.5	12.5	12.5	12.5	12.4	12.4	12.4	12.3	12.3	12.3
	Score		82	82	79.5	78.5	76.5	75.5	74	74	73.5	73.5	72.5	72.5	72	71	71	70.5	70	70	69.5			69	69	68.5	68.5	68.5	68	68	67.5
	Result No.		1	7	m	4		9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22				26	27	28	29

annexin II - rat probable ubiquinon	endoplasmic reticu glucose-regulated	protein kinase ppk	heat shock protein	proteoglycan core	aggrecan - bovine	malate oxidoreduct	RNA-directed RNA p	hypothetical prote	hypothetical prote	transcription fact	liver regeneration	annexin II - bovin	transcription regu
S33700 F82366	A29317 A53211	S51358	A57513	A39808	T42630	A82232	RRXSIB	T34081	T16580	A54025	A39382	LUBO36	B86850
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339	802	804	828	1340	2327	588	878	1130	13055	181	181	339	224
12.3	12.3	12.3	12.3	12.3	12.3	12.2	12.2	12.2	12.2	12.1	12.1	12.1	12.0
67.5	67.5	67.5	67.5	67.5	67.5	67	67	67	67	66.5	66.5	66.5	99
30 31	32	3 t	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 RESULT 1 AH2067 .two-component hybrid sensor and regulator all2094 [imported] - Nostoc sp. (strain PCC 712
C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accebsion: Anzoo, A.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. Por, D., Por, Por, Por, Por, Por, Por, Por, Por
Aritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A; Status: parto: A; Molecule type: DNA
 A;Residues: 1-571 «KUK» A;Cross-references: UNIPROT:QSYV87; UNIPARC:UP100000CE2FB; GB:BA000019; PIDN:BAB73793.1; A;Experimental source: strain PCC 7120 C;Genetics:
A,Gene: all2094
Query Match Best Local Similarity 24.2%; Pred. No. 2.4; Matches 24; Conservative 17; Mismatches 38; Indels 20; Gaps 3;
Qy 23 WGLNTEYD-NLLFVINSIKQEIVNRVQNPRDERGPUMGQKLEILIKD 68
Db 172 WQFDDAQDRNLTEVVQLIDEQTLNSIQNPIISAIQKETTVYLGDGLSPTVGHRIMLITKD 231
Qy 69 TLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPPSK 107
Db 232 GTMIPVADSATPLRNNNGDITGAVWVFRDDTQR 264
DECTT 7

hypothetical protein KIAA0528 - human

C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 31-Dec-2004
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 31-Dec-2004
C;Accession: T00072
C;Accession: T00072
DNA Res. 5, 31-39, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. IX. The complete A;Reference number: Z14086; MUID:98290845; PMID:9628581

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-902 <NAG>
A;Cross-references: UNIPROT:060280; UNIPARC:UPI0000178FFB; EMBL:AB011100; PIDN:BAA25454.1
A;Experimental source: brain; clone HG2576
G;Genetics:
A;Note: KIAA0528

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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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A;Cross-references: UNIPROT;Q12080; UNIPARC:UPI000013BD31; EMBL:Z73502; NID:g1370311; PII A;Experimental source: strain S288C (AB972) H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; submitted to the EMBL Data Library, December 1995 hipmitted to the EMBL Data Library, December 1995 hipmitted to the EMBL Data Library, December 1995 hipmitted to the Sequence of Saccharomyces cerevisiae chromosome XVI left arm. A;Reference number: S69040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Rolecule type: DNA
A, Residues: 1-455 < HAL>
A, Residues: 1-455 < HAL>
A, Residues: 1-455 < HAL>
A, Residues: 1-455 < HAL>
A, Residues: 1-455 < HAL>
A, Residues: 1-455 < HAL>
A, Cost-references: UNIPARC: UPI000013BD31; EMBL: U43703; NID: g1244769; PID: g1244771; MIPS: R, Purnelle, B.; Comblez, S.; Coster, F.; Naveau, F.; Goffeau, A.
Submitted to the EMBL Data Library, March 1996
Submitted to the EMBL Data Library, March 1996
A, Description: The sequence of 55 kb on the left arm of yeast chromosome XVI identifies in the human phosphotyrosyl phosphatase activator PTPA and a homologue to the plant A; Reference number: S69428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,4-alpha-glucan branching enzyme [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI000013BD31; EMBL:X96770; NID:g1403537; PID:g1403563
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                                                                                                                      72
                                                                                                                                                          hypothetical protein YPL146c - yeast (Saccharomyces cerevisiae)
NANternate names: hypothetical protein P2610
NANternate names: hypothetical protein P2610
C,Species: Saccharomyces cerevisiae
C,Species: 3accharomyces cerevisiae
C,Date: 10-Dec-1994 #sequence revision 31-May-1996 #text_change 31-Dec-2004
C,Accession: S65157; S69041; S69453
R,Purnelle, B, Coster, F.; Goffeau, A.
B,Danitted to the Protein Sequence Database, May 1996
A,Reference number: S65154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 KKKAQYEANKVK------LWGLNTEYDNLLFVINSIKQEIV-----NRVQNPR
                                                                                                                      21 KLWGLNTEYDNLLFVIN-SIKQEIVNRVQNPRDER----GPNMGQKLEILIKDT---LGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Gaps
                                                                Gaps
                                                                23; Indels 15;
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Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: SGD:S0006067
A;Map position: 16L
C;Superfamily: tumor suppressor protein, Gltscr2/p60 type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
      DB 2;
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24.8%; Pred. No. 6.7;
tive 21; Mismatches
      ch 14.2%; Score 78.5; DE Similarity 31.6%; Pred. No. 2.3; 24; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                 : : || :|: |
84 EIDLKYSEILNEKFGK 99
                                                                                                                                                                                                                                                          73 PVAGQTSEFVNQVLEK 88
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-455 <PUW>
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            Query Match
Best Local &
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A;Experimental source: strain B31
C;Superfamily: dimethyladenosine transferase (rRNA adenosine dimethyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CjAccession: E70173
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Hanson, M.; Vugt, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Sowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: Smith, H.O.; Venter, J.C.
A;Authors: A70100; MUID:98065943; PMID:9403685
A;Accession: E70173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown protein T6L1.9 [imported] - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C,Accession: F96713
R,Fachologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anture 408, 816-820, 2000
A;Authors: Hunter, J.L.; Yr; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.C., Li, J.J., J.H., Li, Y.; Liu, X.; Liu, Z.H.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. B.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: F96713
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                                                                                                                                                                                                368 RLCRLKKKAQABANA-----TAISNLLPFMEYEVHTQLMNKLK----LKGMNALFGLR 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
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C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 RLKKKKAQY-----EANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQ-----NPRD
                                                                                                                                          5 RACRLKKKAQYEANKVKLWGLNTEYDNLL-FVINSIKQEIVNRVQNPRDERGPN--MGQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
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                      14.9%; Score 82; DB 2; Length 902; 28.4%; Pred. No. 4.3; ive 22; Mismatches 27; Indels
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                                                                                                                                                                                                                                                                                                          62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
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                                                                                         29; Conservative
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Best Local Similarity
Matches 34; Conserv
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A; Residues: 1-281 < KLE>
                                                                Similarity
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A,Map position: 1
                                Query Match
Best Local S:
Matches 29
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. Strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2282
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
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                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q49689; UNIPARC:UPI000016FA8B; EMBL:U00013; NID:g466868; PID:
A;Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z16918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 202-481, A, 483-589 <PAR>
A;Cross-references: UNIPARC:UPI000016FB03; EMBL:Z99125; NID:g2398683; PIDN:CAB16172.1; PJ
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Moseidues 1-1104 «KUR»
Moseidues 1-1104 «KUR»
A;Kesidues 1-1104 «KUR»
A;Cross-references: UNIPROT:QSYQL2; UNIPARC:UPI0000126F6F; GB:BA000019; PIDN:BAB75508.1;
A;Experimental source: strain PCC 7120
C;Genetics:
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Cispecies: Homo sapiens (man)
Cispecies: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
Ciscession: S60255
Cistension: S60255 R.M.
Nature 377, 454-457, 1995
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submitted to the EMBL Data Library, November 1993 A; Description: Mycobacterium leprae cosmid B1496. A; Reference number: S72695
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27.5%; Pred. No. 39;
tive 12; Mismatches
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Best Local Similarity
                                                                                                                                                               A; Accession: S72760
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-869 <SMI>
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A;Status: preliminary
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C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Accession: A65983
R; Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HG
R; Davies, R.M.; Devlin, K.M.
R; Davies, R.M.; Rheherford, K.M.
Nature 409, 1007-1001, 2001
A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq.
A; Reference number: A86909; MUID:21128732; PMID:11234002
A; Accession: A86909; MUID:21128732; PMID:11234002
          k;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA'
A;Residues: 1-642 «KUR»
A;Cross-references: UNIPROT:Q97QS8; UNIPARC:UPI0000C9CBF; GB:AE005672; PIDN:AAK75232.1;
A;Experimental source: strain TIGR4
                                                                                                                                                                                                                                                                         A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916 AAccession: 695129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residuss: 1-869 <STO>
A;Crosetics:
C;Genetics:
A;Gene: ML0593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LKKKAQYEANKVK-----LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pps1 protein - Mycobacterium leprae
N,Alternate names: B1496_C2_189 protein
C;Species: Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Bate: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72760; T11013
R;Smith, D.R.; Robison, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 RIKKKAQYBANKVKLWGLN---TEYDNLLFVINSIKQBIVNRVQNPRDERGPNMGQKLBI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GQKLEILI-----KD-TLGLPVAGQTSEFVNQVLEK 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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C;Superfamily: 1,4-alpha-glucan branching enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%; Score 75.5; Di
Local Similarity 27.6%; Pred. No. 13;
tes 29; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TYDRLGIPDAEKQRLVAGVAAQYESEVV 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Conservative
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A;Cross-references: UNIPARC:UPI000016BAEB; EMBL:X71013; NID:g287944; PIDN:CAA50332.1; PII
                   C,Superfamily: 1,4-alpha-glucan branching enzyme C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: protein B208.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * ||:||: ||
452 IITKLDILVTELLG 465
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Best Local Similarity 25.78
Matches 19; Conservative
                                                                                                                            Best Local Similarity 31.0%
Matches 26; Conservative
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A; Residues: 6-505 < GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: JN0760
A,Molecule type: mRNA
A,Residues: 1-505 <PEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Residues: 1-718 <SCH>
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: NCSP: B208.200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
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C;Superfamily: myo-inositol-1-phosphate synthase
C;Keywords: intramolecular lyase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:Q8DPS6; UNIPARC:UPI00000E3597; GB:AE007317; PIDN:AAK99833.1;
C;Genetics:
-A;Gene: g1gB
                                                                                                   A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1495 <CHE>
A;Residues: 1-1495 <CHE>
A;Cross-references: UNIPROT:Q9Y618; UNIPARC:UPI000016A25F; EMBL:U37146; NID:g1045654; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q96348; UNIPARC:UPI000017952A; EMBL:U66307; NID:g1513227; P1
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A,Title: A transcriptional co-repressor that interacts with nuclear hormone receptors. A,Reference number: S60255; MUID:96008552; PMID:7566127
A,Accession: S60255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4-alpha-glucan branching enzyme (EC 2.4.1.18) [imported] - Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cybate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change U9-Jul-20U4
CyAccession: B98000
Ry Accession: B98000
Ry Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.;
R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, Y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A,Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A,Title: Genome of the Bacterium Streptococous pneumoniae Strain R6.
A,Reference number: A97872; MUID:21429245; PMID:11544234
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                                                                                                                                                                                                                                                                                                                                                          96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Hussain, A.; Bourgeois, J.; Polvi, S.; Tsang, E.; Keller, W.A.; Georges, F. submitted to the EMBL Data Library, August 1996
A;Reference number: 216418
A;Accession: T08436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Streptococcus pneumoniae
Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Brassica napus (rape)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08436
                                                                                                                                                                                                                                                                                                                                                          37 NSIKOEIVNRVQNPRDERGPNMGQKLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                           Query Match 13.3%; Score 73.5; DB 2; Length 1495; Best Local Similarity 30.6%; Pred. No. 57; Matches 22; Conservative 14; Mismatches 17; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nositol-3-phosphate synthase (EC 5.5.1.4) [similarity] - rape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 26.8*
Matches 26; Conservative
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GSITKGIPSTRV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 GLVGLRIPTSKV 108
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A;Molecule type: DNA
A;Residues: 1-642 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-509 <HUS>
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NyAlternate names: F1-F0 ATPase beta chain
(Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 31-Dec-2004
C;Accession: JN0760; S32130; S64699
B;Pena, P; Garesse, R.
Biochem. Biophys: Res. Commun. 195, 785-791, 1993
A;Title: The beta subunit of the Drosophila melanogaster ATP synthase: cDNA cloning, amir A;Reference number: JN0760; MUID:93384603; PMID:8373413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T49572
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Bischulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, R;Schulte, U.; Aign, V.; Hoheisel, Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Gross-references: UNIPROT:Q9P5Z7; UNIPARC:UP1000069977; EMBL:AL355930; GSPDB:GN00116; A.Experimental source: BAC clone B208; strain OR74A
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H
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C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 6
A;Introns: 45/3; 152/1; 274/1; 658/3
C;Superfamily: Schizosaccharomyces pombe negative regulator of mitosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   related to SHK1 KINASE-BINDING protein [imported] - Neurospora crassa
                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
   Length 642;
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                                                                 Indels
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                                                                                                                                   22 LWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNM--
   DB 2;
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13.2%; Score 72.5; D
31.0%; Pred. No. 26;
Live 12; Mismatches
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-----VLEKTAEGNPTGGLVGLRIPTSK 107
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A;Cross-references: FlyBase:FBgn0010217
A;Introns: 22/1; 125/3
A;Introns: 22/1; 125/3
A;Introns: 22/1; 125/3
A;Introns: 22/1; 125/3
A;Introns: 22/1; 125/3
A;Introns: 22/1; 125/3
A;Introns: 22/1; 125/3
A;Introns: 22/1; 125/3
A;Introns: 22/1; 125/3
C;Superfamily: H(*)-transporting ATP synthase; H+-transporting ATP synthase beta chain #status predicted <MAT>
F;205/Product: H+-transporting ATP synthase beta chain #status predicted <MAT>
F;209-384/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
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A;Introns: 94/3; 124/3; 150/3; 209/3; 248/3; 311/3; 424/3; 734/2; 934/2; 1104/3; 1167/3
        R;Pena, P.; Ugalde, C.; Calleja, M.; Garesse, R.
Biochem. J. 312, 887-897, 1995
A;Title: Analysis of the mitochondrial ATP synthase beta-subunit gene in Drosophilidae:
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A;Molecule type: DNA
A;Residues: 1-1355 <WIL>
A;Cross-references: UNIPARC:UFI000017BCEF; EMBL:292788; PIDN:CAB07214.1; GSPDB:GN00019;
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A;Molecule type: DNA
A;Redidues: 1-1555 < WILL
A;Redidues: 1-1555 < WILL
A;Coss-references: UNIPAC: UDIO00017BCEF; EMBL: Z93398; PIDN: CAB07724.1; GSPDB: GN00019; A;Experimental source: clone ZK1151
                                                                                                                                                                                                                                                       A;Cross-references: UNIPARC:UP1000012643F; EMBL:X86015
C;Comment: This enzyme catalyzes the synthesis of ATP coupled to H+ gradient generated
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C.Accession: T22552; T27703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 IVNRVQNPRDERGP------NMGQKLEILIKDTLGLPV------
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llarity 24.4%; Pred. No. 90;
Conservative 21; Mismatches 37; Indels 10; Gaps
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12.9%; Score 71; DB 2; Length 505;
Best Local Similarity 24.8%; Pred. No. 27;
Matches 31; Conservative 11; Mismatches 21; Indels
                                                                                                                     A,Reference number: S64699; MUID:96128076; PMID:8554535
A,Accession: S64699
A)Status: preliminary
A,Molecule type: DNA
A,Residues: 1-505 <PE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ZK1151.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Harris, B.
submitted to the EMBL Data Library, March 1997
A;Refesten number: 220408
AAccession: T27703
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Q6a052 mus musculu
Q7tps5 mus musculu
Q8c0ul mus musculu
Q8c0ul mus musculu
G8cd8 pongo pygma
Q7mf2 gloeobacter
Q8yv87 anabaena sp
Q7z619 homo sapien
C86y87 homo sapien
C86y87 homo sapien
Q86y87 homo sapien
Q86y81 homo sapien
Q72xW0 xenopus lae
Q9c80ul muscula bu
Q7xw0 xenopus lae
Q5c3b borrelia bu
Q73xw0 xenopus lae
Q54xt2 bacteroides
Q8xt2 bacteroides
Q8xt2 bacteroides
Q8xt3 fusobacteri
Q12080 saccharomyc
Q7xvx7 brachganio
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1 KLAPRACRLKKKKAQYEANKV......TABGNPTGGLVGLRIPTSKV 108
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Q80VA1_MOUSE
Q8C1D5_MOUSE
Q6A052_MOUSE
Q7TPS5_MOUSE
Q8C0U3_MOUSE
Q5RDC8_PONEY
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060280_HUMAN
096509_HUMAN
072XW0_XENLA
09CABO_ARATH
KSCA_BORBU
0738A9_BACCI
064XT2_BACFR
08966_TBDV
0898RR3_FUSNU
V246_YEAST
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Q8YV87_ANASP
Q7Z619_HUMAN
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Q7QG21_ANOGA
Q5D9Y2_SCHJA
Q9VC61_DROME
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Q5HYK0_HUMAN
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0443N6_CIOIN 08H0EB_LITER GLGB_STRPN GLGB_STRPN G443N5_CIOIN 0743N5_CIOIN 079SBB_BACRE 079WSBB_BACRE 0600UI_MYCHY 0600UI_MYCHY 0600UI_MYCHY 0618X1_KLEPN Y593_MYCLE 0648BF_STAHJ 041N4Q7_THEPA CARB_ANASP	ated) ated) t sequence upda t annotation up traniata; Verteh ilres; Primates Grouse L.H.; J Grouse L.H.; J Grow K.H.; Schaen Grow K.H.; Schaen T.; Max S.I.; R T.; S.J.; Myerr T.; Max S.J.; Myerr T.; Max S.J.; Myerr T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Max S.J.; Myer T.; Myer T.; Myer T.; Myer T.; Myer T.; Myer T.; Myer T.; Myer T.; Myer T.; Myer T.; My	Score 543; DB 2; Le Pred, No. 7.8e-44; 0; Mismatches 1;
0010000000000	XY; 23, CZ 23, DG 23, DG 25, LG 25, LG 26, LG 27, DG 21, DG 21, DG 21, DG 22, DG 23, DG 24, DG 24, DG 26, DG 27, D	98.5%; 99.1%; ive
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                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                          KLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CS7BL/6J; TISSUE=Testis; MEDLINE=992792783; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4932441F15 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
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                              61 KLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                                                                Length 639;
                                                                                                                                                                                                                                                                                                               Query Match 97.3%; Score 536; DB 2; Length 63 Best Local Similarity 98.1%; Pred. No. 3.7e-43; Matches 106; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                      [1]

NUCLECTIDE SEQUENCE.

Li F., Yao K.T.;

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY139008; AAN28956.1; -; mRNA.

InterPro; IPR004827; TF bZIP.

InterPro; IPR004827; TF bZIP.

PROSITE; PS00365; BZIP. BASIC;

NATH
                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640 AA
                                                                                                       639 AA
                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                          U1-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26, 24,1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBCDGS MOUSE PRELIMINARY;
QBCDGS;
                                                                                                       OBIZGI_HUMAN PRELIMINARY;
                                                                                                                                                          Adult retina protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
Name=A930001N09Rik;
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                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                             HUMAN
                                                                                  RESULT 2
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RA ddachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Phuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., RA Hayashida K., Imotani K., Ishii Y., Itoh M., Kagawa I., Kabukawa T., Ra Hori P., Imotani K., Ishii Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tomaru A., Takahal-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., EMBL, AKOJOO92; BACCEOTO I. MINA.
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whinhaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotation of a full-length mouse cDNA collection.";
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Pred. No. 9.8e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Testis;
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93.5%;
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"Functional anno
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1 KLAFRACRLKKKKAQYEANKVKLMGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ 60
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skali Z., Cattolico L., Poulain J., De Berardinis V., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff JW., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Quigo R., Saurin W., Scarpelli C., Wincker P., Lander B.S., Weissenbach J., Roest Crollius H., "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511 TLEHLIQQTLGENPFRRDSQQNQTIFSQKRKVNDVNVDLKYILKHFSLSPQVAPPVAGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KLEILIKDTLG------LPVAGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
Anophelinae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope, Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.0%; Score 352.5; DB 2; Length 600; 51.3%; Pred. No. 2e-25; ive 13; Mismatches 17; Indels 43
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600 AA; 66291 MW; B2F28B2F3B27B1C4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 SEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Committee;
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ORFNames=ENSANGG0000012681;
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NON TER
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                   1 KLAFRACRIKKKKAQYEANKVKLWGLNTEYDNILFVINSIKQEIVNRVQNPRDERGPNMGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLAFRACRLKKKKAQYBANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGPNMGQ
                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OKFNames-GSTENGO0029962001;
Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Tetraodon nigroviridis (Green puffer).
Actinopterygii, Neopterygii, Teleostei, Euteleostei;
Acanthomorpha; Acanthopterygii, Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The German CDNA Consortium;

Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,

Fobo G., Han M., Wiemann S.;

Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

EMBL; BX647573; CAI46104.1; -; mRNA.

InterPro; IPR004827; TF bZIP.

PROSITE; PS000135; BZIP_BASIC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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0
                                                                                                                                                                                                                                             KLEILIKDTLGLPVAGQTSEFVNQVLGKTAEGNPTGGLVGLRIPASKV 640
                                                                                                                                                                                                          61 KLEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRIPTSKV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          604 AA; 68572 MW; 977C229B63E2E4C2 CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 7 SCAP15001, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-WAY-2005 (TrEMBLrel. 30, Created)
10-WAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Hypothetical protein DKFZp313F2319 (Fragment).
Name=DKFZp313F2319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 64.1%; Score 353; DB 2; Local Similarity 97.2%; Pred. No. 1.8e-25; nes 69; Conservative 1; Mismatches 1;
                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              QSHYKO_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q4RRX3_TETNG PRELIMINARY;
                            Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 KLEILIKDTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
TISSUE=Adipose;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=99883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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SEQUENCE
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ð 8 Best Loc Matches

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 KLASKICRLKKKAFHEANKIKYLGLEIEYNELASVIVRIKELITKYL---RDHLPP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KLAFRACRLKKKAQYEANKVKLWGLNTEYDNLLFVINSIKQEIVNRVQNPRDERGP 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The full-length cDNA sequences of Schistosoma japonicum genes."; Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
BNBL; AY815642; AAW27374.1; -; mRNA.
Hypothetical protein.
SEQUENCE 584 AA, 65536 MW; 3E5055EF335323CC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 20.6%; Score 113.5; DB 2; Length 584; Local Similarity 50.0%; Pred. No. 0.028; Onservative 6; Mismatches 19; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                            21.8%; Score 120; DB 2; Length 293; 79.3%; Pred. No. 0.003; tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
10-WAY-2005 (TrEMBLrel. 30, Last annotation update)
CG13624-PA, isoform A (Cg13624-pb, isoform b) (SD09792p)
                                            293 293
293 AA; 31535 MW; 0700521A3C593F97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           10-MXY-2005 (TrEMBLrel. 30, Created)
10-MXY-2005 (TrEMBLrel. 30, Last sequence update)
10-MXY-2005 (TrEMBLrel. 30, Last annotation update)
Hyporhetical protein.
Schistosoma japonicum (Blood fluke).
                                                                                                                                                                                                                                                                                                                                                                         584 AA
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                                                                                                                                                                                                                                     247 KLASRACRLKKKAQHEANKIKLYGLETEH 275
                                                                                                                                                                                                           1 KLAFRACRLKKKAQYEANKVKLWGLNTEY 29
  PS00036; BZIP_BASIC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                            Query Match
Best Local Similarity 79.34
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                     OSD9Y2_SCHJA PRELIMINARY;
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Q9VC61; Q8T9A9;
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NUCLEOTIDE SEQUENCE.
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PROSITE; I
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SEQUENCE
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Matches
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Produce No. 1, Norther A., Denge S., Way A.D., Dong T., Dieter S. M., Dodgen P., Dourbou E.S. Bowenes C., Fortactes S., Picklemann M., Colled A., Good F., Gorell J.H., Gw. Dougher M., Glasser K., M. Bartish K.J., Harvey D.A., Heiman T.J., Hermander J.R., Houck J., Charlellan A.B., Garg N.S., Galbart W.M., Glasser K., M. Harrish M.J., Harvey D.A., Heiman T.J., Hermander J.R., Houck J., M. Harrish M.J., Harvey D.A., Heiman T.J., Hermander J.R., Houck J., M. Harrish M.J., Harvey D.A., Heiman T.J., Hermander J.R., Houck J., M. Harrish M.J., Harvey D.A., Heiman T.J., Hermander J.R., Man W. Y., Malon F. W., Man M. J., M. Harrish M.J., Kalmander J.R., Man W. J., Malon D.R., Wallon D.L., Malon M.J., Marthy D.M., Wallon D.M., Malon D.M., Malon D.M., Malon M. J., Malon D.M., Malon M. J., Malon D.M., Malon M. J., Malon D.M., Malon M. J., Malon D.M., Malon M. J., Malon D.M., Malon M. J., Malon D.M., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon D.M., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon D.M., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Malon M. J., Mal
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5 RACRIKKKAQYEANKVKIMGINTEYDNIL-FVINSIKQEIVNRVQNPRDERGPN--MGQK 61
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
              EMBL; BC049905; AAH49905.1; -; mRNA.
Ensembl; ENSMUSG0000030279; Mus musculus.
MGI; MGI:1921991; 5730419109Rlk.
                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                     SEQUENCE
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                                                                                                                      Query Match
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Q8CID5_MOU
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TISSUB-MARMMARY thouse. Metallothionien-TGF alpha model. 10 month old

Virgin mouse. Taken by blopsy.;

XX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

XX Atausner R.D., Collins F.A., Grouse L.H., Derge J.G.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XA Altschul S.F., Zeeberg B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XA Altschul M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,

XA Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,

XA Brownstein M.J., Wekman F.B., Poters G.J., Abramson R.D., Mullahy S.J.,

XA Richards S., McCwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

XA Wilting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

XA Richards A.C., Grimwood J., Schmutz J., Myers R.M.,

XA Richards A.C., Grimwood J., Schmutz J., Wyers R.M.,

XA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,

XA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

XA Mannan A., Schein J.E., Jones S.J.M., Marra M.A.;

XA Mannan A., Schein J.E., Jones S.J.M., Marra M.A.;

XA Mannan A., Schein J.E., Jones S.J.M., Marra M.A.;

XA Mannan A., Schein J.E., Jones S.J.M., Marra M.A.;

XA Mannan A., Schein J.E., Jones S.J.M., Marra M.A.;

XA Mannan A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy.;
Strausberg R.;
                   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                               20.5%; Score 113; DB 2; Length 755; 75.9%; Pred. No. 0.041;
                                                                                                                                            Q9VL14:CG18619; NbExp=1; IntAct=EBI-150517, EBI-165049;
                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                     EMBLY, 09VC61;

Ensembl; CG13624; Drosophila melanogaster.

Ensembl; CG13624; Drosophila melanogaster.

Elybases; Esgn0032929; CG13624.

InterPro; IFR004827; TF b2IP.

PROSITE; PS00036; BZIP BASIC; UNKNOWN I.

PROSITE: A. R2263 MW; D851D42235FF10E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    708 KLASRACRLKKKAQHEANKIKUFGLEIEH 736
                                                                                                                                                            EMBL; AE003748; AAF56314.2; -; Genomic_DNA
EMBL; AY069850; AAL39995.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                    1 KLAFRACRLKKKAQYEANKVKLWGLNTEY 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5730419109Rik protein (Fragment).
Name=5730419109Rik;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBOVAL MOUSE PRELIMINARY;
QBOVAL;
                                                                                                                                                                                                                                                                                                                   Query Match 20.5
Best Local Similarity 75.9
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
          NUCLEOTIDE SEQUENCE
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                                                                                                                          -1- INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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a programme and the second

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CSTRAIN=EVUBNIN; TISSUD=Mammary tumor. C3;

KEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAURDERG R.L., Ferimond B.A., Grouse L.H., Derged J.G.,

RIGHORIS R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hashe F.,

Detchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

As tapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahe J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Buterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

And Montan A., Schein J.E., Jones S.J.M., Marra M.A., F., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Shore C.D., Sh
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                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                        5 RICRIKKKAQAEANA-----TAISNILPPMEYEVHTQLMNKIK----LKGMNALFGLR 53
                                                                                                                                                                                                                                                                                5 RACRLKKKAQYEANKVKLWGLNTEYDNLL-FVINSIKQEIVNRVQNPRDERGPN--MGOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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15.8%; Score 87; DB 2; Length 818;
Best Local Similarity 29.4%; Pred. No. 15;
Matches 30; Conservative 22; Mismatches 26; Indels
                                                                            15.8%; Score 87; DB 2; Length 487; 29.4%; Pred. No. 8.3; tive 22; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FVB/N; TISSUE=Mammary tumor. C3; Director MGC Project; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC027763; AAH277763.1; "; mRNA. Ensembl; ENSMUSGO000030279; Mus musculus. MGI; MGI:1921991; 5730419109Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
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487 AA; 53277 MW; 9CE3489ADD52AAC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 IQITVGETMLMGLASATGVYLAAL-----PTPG--GIQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nd mouse cDNA sequences.";
roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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01-MAR-2003 (TEMBLIE). 23,
01-MAR-2004 (TEMBLIE). 26,
RIKEN CDNA 5730419109.
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QBCIDS;
01-MAR-2003 (TrEMBLIEL: 23
                                                                                                                                                                                               30; Conservative
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Mus musculus (Mouse)
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CSTRAINE-CSTBL/GST TISSUE-ERG9;

KN STRAINE-CSTBL/GST TISSUE-ERG9;

KN STRAINE-CSTBL/GST TISSUE-ERG9;

KN STRAINE-CSTBL/GST;

PubMed=12477932; DOI=10.1073/pnas.242603899;

KN STAUBDETG R.L., Felingold R.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Wagner L., Shemen C.M., Schuler G.D.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hatch R.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hatch F.,

A patchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Kilalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Rahakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Reneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 RACRLKKKKAQYEANKVKLWGLNTEYDNLL-FVINSIKQEIVNRVQNPRDERGPN--MGQK 61
Name=5730419109Rik;
Mus musculus (Mouse).
Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
Muroidea; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.8%; Score 87; DB 2; Length 1016; 29.4%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUE=Egg;
Strausberg R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1016 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QEC013 MOUSE PRELIMINARY;
QBC013;
01-MAR-2003 (TEMBLrel. 23,
01-MAR-2003 (TEMBLrel. 23,
01-MAR-2004 (TEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Conservative
                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
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ID Q8
AC Q8
DT 01
DT 01
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A Nagase T., Ohara O., Koga H.;

The complete nucleotide sequences of mouse homologues of KIAA gene:

I. The complete nucleotide sequences of 500 mouse KIAA-homologous

The complete nucleotide sequences of cona clones

The complete nucleotide sequences of cona clones

The complete nucleotide sequences of cona clones

The conplete nucleotide sequences of cona clones

The Result Sampled from size-fractionated libraries.";

DNA Res. 11:205-218(2004).

- SIMILARITY: Concains 1 C2 domain.

Embl., AKI7266; BAD32244.1; -; RRNA.

BRBL, AKI7266; BAD32244.1; -; RRNA.

BRBL, AKI7266; BAD32244.1; -; RRNA.

Co. GO:0016220; C:membrane; IEA.

GO; GO:0016220; C:membrane; IEA.

GO; GO:0006215; Firansporter activity; IEA.

RO; GO:0006215; Firansporter activity; IEA.

RITHERPEO; IPRO00008; C.:

RITHERPEO; IPRO00008; C.:

RITHERPEO; IPRO00008; C.:

RITHERPEO; IPRO00008; C.:

RITHERPEO; PROMO0008; C.:

RITHERPEO; PROMO0008; C.:

RITHERPEO; PROMO0008; C.:

RITHERPEO; PROMO0008; C.:

RITHERPEO; PROMO0008; C.:

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RITHERPEO; PROMO0008; C.:

RITHERPEO; PROMO0008; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 RACRIKKKAQYEANKVKIMGINTEYDNIL-FVINSIKQEIVNRVQNPRDERGPN--MGQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroldea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.8%; Score 87; DB 2; Length 993; 29.4%; Pred. No. 18; ive 22; Mismatches 26; Indels
                                                                                                              368 IQITVGETMLMGLASATGVYLAAL-----PTPG--GIQI 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
                                                                              62 LEILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     560 IQITVGETMLMGLASATGVYLAAL-----PTPG--GIQI 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 993 AA; 109096 MW; 9C7853BC7E8085C6 CRC64;
                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
MIRA0528 protein (Fragment).
Name=5730419109R1k; Synonyms=mKIAA0528;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                           993 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50004; C2 DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGMN.
SWART; SM00239; C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT_2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 29.48
Matches 30; Conservative
                                                                                                                                                                                                                                                 QGA052_MOUSE PRELIMINARY;
QGA052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7TPSS_MOUSE PRELIMINARY;
Q7TPSS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5730419I09Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fetal brain;
PubMed=15368895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Q7TPS5 MOUSE
1D Q7TPS5 MC
AC Q7TPS5, MC
DT 01-OCT-20
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KRAIN-C57BL/63. TISSUB-Testis;

KX KAWAIN-C57BL/64: TISSUB-Testis;

KX KAWAIN-C57BL/64: TISSUB-Testis;

KX KAWAIN-C57BL/65: PubMed=11217851; DOI=10.1038/35055500;

KX KAWAIN-C57BL/64: TISSUB-Testis;

KA Arawaw T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kaudawa T., Saito R.,

RA Aizawa K., Izawa M., Nishi K., Goodo S., Yamanaka I.,

RA Aizawa K., Matsuba H., Ashburner M., Batalov S., Casavant T.,

RA Aizawa K., Staubli F., Suzuki K., Tomita M., Magner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N.,

Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Wymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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NUCLECTIDE SEQUENCE.

STRAIN=C57BL/6J; TISSUE=Testis;

STRAIN=C57BL/6J; TISSUE=Testis;

A Sibate K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., A Yamamoto R., Mateumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Tanaka T., Danaka T., Danaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rukiki integrated sequence analysis (RISA) system-384-format gequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STEATN=C57BL/63; TISSUE=Testis; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazahi Y., Muramateu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493058816 product:hypothetical C2 domain/C2-domain profile/Synaptoctagmin/Cytochrome c family heme-binding site containing protein, full insert sequence.
Name=5730419109Rik;
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=Testis; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Rayashizaki Y.; Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Testis;
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                                                                                                                                       (Mouse)
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                       Mus musculus
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                    Adachi J. Aizawa K. Akimura T., Arakawa T., Bono H., Carninci P., Adachi J. Aizawa K. Akimura T., Hara A., Hashizume W., Adachi J. Aizawa K. Akimura T., Hara A., Hashizume W., Bukuda S., Furuno M., Hanagaki T., Haracka T., Hirozane T., Hayashida K., Hayatsu N., Hiranaco K., Hiracka T., Hirozane T., Aracka J., Kojima Y., Kondo S., Konno H., Kouda M., Kaya S., Katch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Satch H., Sakazume N., Sano H., Sasaki D., Saitoh H., Sakai C., Sakazume N., Sano H., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EmBL/GenBank/DDBJ databases.

S. EmBL, AKOS925; BAC26634.1; -; mRNA.

B. Ensembl; ENSWUSG0000003025; Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         517 RLCRIKKKAQABANA-----TAISNILPFMBYBVHTQLMNKLK----LKGMNALFGLR 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 RACKLKKKAQYEANKVKLWGLNTEYDNLL-FVINSIKQEIVNRVQNPRDERGPN--MGQK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S., Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1016 AA; 111684 MW; CA8958E385587E0B CRC64;
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1-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Hypothetical protein DKFZp46900513.
Name=DFZp46900513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.4%; Score 85; DB 2;
30.9%; Pred. No. 30;
tive 19; Mismatches 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1000 AA.
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GO:0005215; P:transporter activity; IEA.
GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI; MGI: 1921991; 5730419109Rik.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0008021; C:synaptic vesicle; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

Interpro; IPR001008; C2.

Interpro; IPR001565; Synaptotagmin.
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EMBL; CR857986; CAH90229.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 LEILIKDTLGLPVAGOTSEFV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50004; C2 DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 30.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00168; C2; 1.
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   SEQUENCE
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NUCLEOTIDE
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QSRDC8
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STRAIN=PCC 7421;
MEDLINE=22977040; PubMed=14621292;
MRABALINE=22977040; PubMed=14621292;
MRABALINE Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T., Sasamoto S., Watanabe A., Kawashina K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of Gloeobacter violaceus PCC 7421, a cyanobacterium that lacks thylakoids.";
DNA Res. 10:137-145(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gloeobacter violaceus.
Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacterales; Gloeobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0001524; F:ATP binding; IEA.

R GO; GO:000155; F:two-component sensor molecule activity; IEA.

R GO; GO:0000165; F:two-component sensor molecule activity; IEA.

R GO; GO:0000160; P:two-component sensor molecule activity; IEA.

R InterPro; IPR003594; ATPbind_ATPase.

R InterPro; IPR003661; His Kin HAMP.

R InterPro; IPR004368; His Kin HAMP.

R InterPro; IPR004368; His Kin HAMP.

R InterPro; IPR00414; PAS.

R InterPro; IPR000700; PAS-assoc_C.

R Pfam; PF00672; HAMP; 1...mp.
                                                                                                                                                                                                                                                                                                                                                         15.2%; Score 84; DB 2; Length 1000; 29.7%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                              31, Indels
                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 1000 AA; 110365 MW; FB307C795DA63C92 CRC64;
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SEQUENCE 718 AA; 78094 MW; D3E695454C0956DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 EILIKDTLGLPVAGQTSEFVNQVLEKTAEGNPTGGLVGLRI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Two-component sensor histidine kinase.
OrderedLocusNames=g110814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                718 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              18; Mismatches
InterPro; IPR001008; C2.
InterPro; IPR001565; Synaptotagmin.
Pfam; PF00168; C2; 1.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00399; SYNAPTOTAGMN.
SMART; SM00239; C2; 1.
PROSITE; PS50004; C2_DOMAIN_2; 1.
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TIGRRAMs; TIGR00229; sensory_box; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50113; PAC; 1.
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Pfam; PF00512; HisKA; 1.
Pfam; PF00989; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 29.7%
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                Query Match
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O7NMF2_GLOVI
O7NMF2_GLOVI
O7NMF2_GLOVI
O7NMF2_G
DT 01-MAR-2
DT 01-MAR-2
DE TWO-comp
OX OX GLOCOGC
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15.0%; Score 82.5; DB 2; Length 718; 24.3%; Pred. No. 35;

Query Match Best Local Similarity

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4
                                        46
                        3 AFRACRIKKKAQYEANKVKLWGINTEYDNLLFVINSIKQEIV------NR----
47; Gaps
45; Indels
                                                                          47 VONPRDERGPNMGOKLEILIKDTLGLPVAGOTSEFVNOVLE----
 20; Mismatches
                                                                                                                             88 -----KTAEGNPTGGLVGLRIPTSK 107
                                                                                                                                                       461 LOITAAPLRIGEGELLGGVAVLRDITAQ 488
                                                                                                                                                                                           Search completed: February 28, 2006, 08:53:06 Job time : 41.609 secs
 36; Conservative
  Matches
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